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OM protein - protein search, using sw model

February 6, 2003, 11:16:00; Search time 27.8333 Seconds (without alignments) 19.150 Million cell updates/sec Run on:

PAT943-1

1 dyda 4 Perfect score: Sequence: **BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

710 Total number of hits satisfying chosen parameters:

908470 seqs, 133250620 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 100% Maximum Match 100%

Database :

A_Geneseq_101002:*

/SIDS2/gcgdata/geneseg/genesegp-embl/AA1989.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1990.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:* /SIDSZ/gcgdata/geneseqp-embl/AA1994.DAT:*/SIDSZ/gcgdata/geneseqp-embl/AA1995.DAT:*/SIDSZ/gcgdata/geneseqp-embl/AA1996.DAT:*/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDSZ/gcgdata/geneseq /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* /SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Thermus thermophil	CDR-2 of the H cha	YadA homologous pe	Alpha-1,3/4-fucosi	Proteobacterial ex	Cyclitol-ubiquinon	Sequence of trypti	Peptide #10124 enc	Human brain expres	Human bone marrow
SUMMAKLES			QI	AAY50026	AAW58532	AAB51592	AAR86991	AAB51521	AAW36471	AAR49685	ABB42618	AAM63509	AAM76323
			DB:	20	19	21	17	21	18	15	22	22	22
			Match Length DB	13	16	19	20	21	23	28	38	38	38
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Peptide #10469 enc Arabidopsis thalia Arabidopsis thalia Staphylococcus aur Streptococcus pneu S. pneumoniae trun Partial D. gossypi Human apoptosis re Propionibacterium Peptide having aff Homo sapiens anti- Clostridium thermo Novel human diagno Peptide #1023 enc Human brain express Human testicular a Sequence encoded b Arabidopsis thalia Human reproductive Staphylococcus epi Human reproductive Staphylococcus epi Human new brain exproductive Staphylococcus epi Human new brain exproductive Staphylococcus epi Human obers stablia Novel human diagno Subtilases EEEPIP fuman ovarian anti	Arabidopsi
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AAM36432 AAG10870 AAW5275 AAW62275 AAW41839 AAW41839 AAW41839 AAW62591 AAW62591 AAW62591 AAW62591 AAW62591 AAW62591 AAW62591 AAW62591 AAW62591 AAW62591 AAW6363 AAW636 AAW6	AAGDI
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ALIGNMENTS

AAY50026 standard; peptide; 13 AA. RESULT 1 AAY50026

AAY50026;

(first entry) 19-JAN-2000

Thermus thermophilus Pol III-type enzyme alpha subunit peptide TTH2.

DNA polymerase III; dnaE gene; alpha subunit; thermostable; DNA synthesis; speed; accuracy; processivity; frameshift; holoenzyme; assembly; exonuclease; proofreading; inverse PCR.

Thermus thermophilus.

W09953074-A1

21-0CT-1999.

98WO-US07070. 09-APR-1998; 98WO-US07070. 09-APR-1998;

(UYRQ) UNIV ROCKEFELLER.

Jeruzalmi O'Donnell ME, Kuriyan J, Yurieva O,

ä

WPI; 1999-611306/52.

New isolated thermostable DNA polymerase III-type enzyme, used particularly for the amplification and sequencing of nucleic acids ${\sf P}$

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pat943-1.rag

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This sequence represents TTH2 peptide, derived from the purified alpha subunit (encoded by the dnaE gene) of a novel Thermus thermophilus calpha subunit (encoded by the dnaE gene) of a novel Thermus thermophilus thermostable DNA polymerase holoenzyme which corresponds to DNA colymerase in the peptide was used to design primers (AAZ30923-Z30924) for PCR of the dnaE gene. Pol III-type caybes have a high processivity (>50 kb) and rapid rate of synthesis (750 nucleotides/s). Pol III consists of 18 subunits of 10 different capha (DNA polymerase) core is the catalytic unit and consists of the alpha (DNA polymerase). Pol III consists of 18 subunits of 10 different care the beta subunit ("sliding clamp") is ring-shaped and encircles DNA and It is the beta subunit which is responsible for the high processivity can speed. The gamma complex (composed of gamma, deltar, deltar, chi and seed. The gamma complex (composed of gamma, deltar, deltar, chi and casembly of beta clamps around DNA. A dimer of the tau subunit acts as a seasombly for beta clamps around DNA. A dimer of the two cores within pol colymerase and one molecule of gamma complex, forming the Pol III*

Colymerase and one molecule of gamma complex, forming the Pol III*

Colymerase and one molecule of gamma complex, forming the Pol III*

Colymerase and one molecule of gamma complex, forming the pol III*

Colymerase and one molecule of gamma complex, forming the pol III*

Colymerase and one molecule of gamma complex, forming the pol III*

Colymerase and one molecule of gamma complex, forming the pol III*

Colymerase and one molecules of gamma complex, forming the pol III*

Colymerase and one molecule of gamma complex, forming the pol III*

Colymerase and one molecules of gamma complex, forming the pol III*

Colymerase and one molecules of gamma complex, forming the pol III*

Colymerase and one molecules of gamma complex, forming the pol III*

Colymerase and one molecules of gamma complex, forming the pol III*

Colymerase and one molecules of gamma complex, forming t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; anti-My-10; H chain variable region; L chain variable region; antibody; heavy; light; CDR; human CD34 antigen; hybridoma; anti-CD34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant antibody against human CD34 - and nucleic acid encoding it, used for efficient production of the antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 13; 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDR-2 of the H chain variable region from mouse anti-My-10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             excise misinserted nucleotides (proofreading)
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100.0%; Pred. No.
Example 10; Fig 15B; 156pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0331647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-391043/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP10155489-A.
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Matches
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The present invention describes a nucleic acid which encodes an anti-My-10 antibody. The present sequence represents the CDR-2 of the H chain variable region of the antibody. Also described is a method for the production of a recombinant antibody in which the above nucleic acid is used to produce an antibody which combines with human CD34 antigen by gene recombination. The anti-CD34 antibody gene is used to produce recombination the anti-CD34 antibody gene is used to produce recombinant anti-CD34 antibody which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved proteobacterial extracellular domains. Sequences AAB5158 - AAB51618 represent peptides homologous to Yadh, a yersinia adhesin which is an important virulence determinant of the Yersinia species. The invention includes an antibody which binds to the proteobacterial extracellular peptides, and an immunogenic composition proteobacteria. The polypeptides and antibodies are useful in the rearment and prevention of proteobacterial infection by a proteobacteria. The polypeptides and antibodies are useful in the can also be used to identify compounds which antagonize the binding of a bacterial adhesion to its ligand. The host cell can be used to produce the polypeptides in a suitable culture system. The composition can be used to vaccinate a patient against a proteobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to peptides AAB51512 - AAB51537 which represent conserved proteobacterial extracellular domains, Sequences AAB51618 represent beptides homologues to vada
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated polypeptide conserved in proteobacterial extracellular domains used in the treatment and prevention of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; extracellular domain; virulence determinant; YadA; adhesin; proteobacterial infection prevention; vaccine.
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                                                                                                                                                                                                 Length 16;
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100.0%; Pred. No. 72;
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86;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         AA.
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100.0%;
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                                                                                                                                                                                                                                  Conservative
                                                                                                                          used in pharmaceuticals.
                                                                                                                                                                      Query Match
Best Local Similarity
4; Conserve
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| DYDA 12
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adhesin; proteobacterial infection prevention; vaccine.
                                                                                                                                                       WPI; 2000-647397/62.
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Best Local Similarity
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                  Yersinia pestis.
                                    WO200061165-A1
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                                                      19-OCT-2000
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                                                                                                                                      Lupas AN;
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                                                                                                                                                      ptomyces; alpha-1,3/4-fucosidase; primer; PCR; amplification; probe;
organism; E.coli; animal; plant; structure; function; sugar chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                       Alpha-1,3/4-fucosidase gene from Streptomyces sp. 142 - useful for recombinant production of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; extracellular domain; virulence determinant; YadA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                     Yuka T;
                                                                                                                                    Alpha-1,3/4-fucosidase pepticde fragment 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23;
ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                    Masanori M, Mutsumi S,
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 16pp; Japanese.
                                                                              AAR86991 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA SHUZO CO LTD
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                                                                                                                   (first entry)
Conservative
                                                                                                                                                                                         Streptomyces sp. 142
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Best Local Similarity
4; Conserve
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                                                                                                                                                     Streptomyces;
host organism
                                                                                                                                                                         glycoprotein.
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                            |||||
10 DYDA 13
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                                                                                                                                                                                                                                              18-MAY-1994;
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10 DYDA 13
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                                                                                                 AAR86991;
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Matches
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ID AAB:
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This invention relates to peptides AAB51512 - AAB51537 which represent conserved proteobacterial extracellular domains. Sequences AAB51618 represent peptides homologous to YadA, a yersinia adhesin which is an important virulence determinant of the Yersinia species. The invention includes an antibody which binds to the proteobacterial extracellular peptides, and an immunogenic composition containing the antibody used as a vaccine to prevent infection by a proteobacteria. The polypeptides and antibodies are useful in the treatment and prevention of proteobacterial infections. The polypeptides can also be used to identify compounds which antagonize the binding of a bacterial adhesion to its ligand. The host cell can be used to produce the polypeptides in a suitable culture system. The composition can be used to vaccinate a patient against a proteobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated polypeptide conserved in proteobacterial extracellular domains used in the treatment and prevention of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidation; cyclitol; cyclitol-ubiquinone oxidoreductase; synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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ilarity 100.0%; Pred. No. 96;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclitol-ubiquinone-oxidoreductase peptide 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= unknown
/note= "encoded by NNN"
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                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 64; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gluconobacter oxidans DSM 50049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ketocyclitol; inosose epimer.
13-APR-2000; 2000WO-US09866.
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Gaps

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Indels

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                   Amylogenin or self glucosylating protein (SGP) is a starch primer. It can be purified from the endosperm of a US inbred line (B73) of Zea mays. The protein was then digested with trypsin in an enzyme/substrate ratio of 1.25 for 15 hr. The tryptic digest was fractionated. Nine of the peptide peaks (labelled P1-P9) were tryptic peptide peaks were obtd. Nine of the purified a number of peptides were chosen for As sequence analyses (labelled tryptic The sequences of these peptides is given in AAR49682-90. The radiolabelled peptide T2 is a proteolytic fragment of the larger radiolabelled peptide T6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #10124 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 35253; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 15;
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB42618 standard; Peptide; 38 AA.
                                    Example; page 35; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0207456.
2000US-0608408.
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2000us-0234687.
2000us-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                  AA;
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17 DYDA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                      1 DYDA 4
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                          - useful for analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                           shown in AAW36454-74 are fragments of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (P4) of sweet corn starch primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plants, esp. maize, having altered starch production ability prepared by inserting into the plant genome an amylogenin gene encoding a starch primer which initiates synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Starch primer; amylogenin; starch synthesis; SGP; maize; sweet corn; self glucosylation protein; tryptic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Singletary GW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 18; 100.0%; Pred. No. 1.1e+02;
                                                                    (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
                                                                                                                                                                                                 Cyclitol-ubiquinone oxido:reductase enzyme synthesis of keto:cyclitol epimers, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J,
                                                                                                                Wissler JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lomako
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR49685 standard; Peptide; 28 AA.
                                                                                                                                                                                                                                                      Claim 5; Page 15; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of tryptic peptide T4 protein designated amylogenin.
96DE-1028873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keeling PL,
                                    95DE-1025990
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                                                                                                             Wiesner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92GB-0018185.
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                                                                                                                                                                                                                                                                                             The peptide sequences
                                                                                                                                             1997-088583/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AA;
                                                                                                                                                            N-PSDB; AAT96623
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                                                                                                         Freivogel KW,
                                    17-JUL-1995;
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17 DYDA 20
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1 DYDA 4

δ Q

Sequence

Query Match

Matches

18-AUG-1994

AAR49685;

26-AUG-1993; 26-AUG-1992;

Whelan WJ;

WO9404693-A

AAR49685
XX
AC AAR4
XX
DT 18-A
XX
DE Sequ
DE Sequ
DE Star
XX
XX
XX
DS Zea
XX
XX
PN W094
XX
XX
XX
XX
PN W01;
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PN W01;
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PN W01;
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PN W01;
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PN W01;
XX

Zea mays.

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RESULT 9 AAM63509

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #10469 encoded by probe for measuring placental gene expression.
                                                                                                                                Human bone marrow expressed probe encoded protein SEQ ID NO: 36629.
                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 36629; 658pp + Sequence Listing; English.
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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                                  AAM76323 standard; Protein; 38
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
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                                                                                                (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                             WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                               Homo sapiens
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19 DYDA 22
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                                                                  AAM76323;
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    RESULT 10
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                     AAM76323
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                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe encoded protein SEQ ID NO: 35614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                  Gaps
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                             Score 23; DB 22;
Pred. No. 1.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                          AAM63509 standard; Protein; 38 AA.
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0
                                                             Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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19 DYDA 22
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19 DYDA 22
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Gaps

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Matches

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Length 38; Indels

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9905-0128714.
9905-0129845.
9905-0130047.
9905-0130449.
9905-0131449.
9905-0131449.
9905-0132484.
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990S-0134256.
990S-0134218.
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990S-0134221.
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9905-0139456
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99US-0135353.
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99US-0143542.
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99US-0136021
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65-MAY-1999

66-MAY-1999

66-MAY-1999

11-MAY-1999

11-MAY-1999

14-MAY-1999

18-MAY-1999

18-MAY-1999
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25-MAY-1999;
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  ö
                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 9365.
                                                                                                                                                                                                                    Claim 27; SEQ ID No 36701; 654pp; English.
                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAG10870 standard; Protein; 41 AA
                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                      04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0508408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000US-023687.
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990S-0123180.
990S-0125548.
990S-0126264.
990S-0126785.
990S-0126785.
                                     2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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Les 4; Conserv
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WO200157272-A2
                                                     04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 2
                                    30-JAN-2001;
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05-MAR-1999;
09-MAR-1999;
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31-AUG-1999;
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.larity 100.0%;
.Conservative 0
           9905 - 0159329
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana

EP1033405-A2.

06-SEP-2000

990S-0121825. 990S-0123180. 990S-0123748. 990S-0125788. 990S-0126745. 990S-0127462. 990S-0128714. 990S-0130077. 990S-0130049. 990S-0130049.

25-FEB-1999; 05-MAR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 06-APR-1999; 06-APR-1999; 16-APR-1999; 119-APR-1999; 21-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999;

2000EP-0301439

25-FEB-2000;

Arabidopsis thaliana protein fragment SEQ ID NO: 68915

(first entry)

18-OCT-2000

AAG54078;

AAG54078 standard; Protein; 41 AA

905-013204 905-013206 905-013248 905-013248 905-013248 905-013248 905-013286 905-013286 905-013286 905-013286 905-013286 905-013286 905-013421	9905 - 0135124, 9905 - 0135629, 9905 - 0135629, 9905 - 0135639, 9905 - 0136392, 9905 - 0137522, 9905 - 0139452, 9905 - 0139453, 9905 - 0139455, 9905 - 0139456, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139462, 9905 - 0139461, 9905 - 0139461, 9905 - 0139461, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139462, 9905 - 0139750	US-0139891 US-0140635 US-0140635 US-0140695 US-014082 US-0141847 US-014205 US-014205 US-014206 US-014305 US-0144086 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335 US-0144335
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1-70L-1999; 2-70L-1999; 2-70L-1999; 2-70L-1999; 2-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999; 3-70L-1999;	04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 10-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 22-AUG-1999; 21-AUG-1999; 22-AUG-1999; 21-AU	-0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999; -0CT-1999;
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surface protein A (PspA) protein from Streptococcus possible and surface protein A (PspA) protein from Streptococcus possible a fusion recombinant DNA molecule has been developed which encodes a fusion protein comprising a truncated form of PspA and cholera toxin B subunit (TTB), where the DNA molecule comprises a nuclectide sequence encoding the truncated PspA inked by an in-frame genetic fusion to a ctxB gene, and where the truncated PspA contains immunoprotective epitopes and up to 90% of the whole PspA protein, except for the cell membrane anchor region. The fusion protein is useful for providing an immunogen to proteins of this strain are not immunogenic enough to provide protection. The antigenic epitopes of the fusion protein are directed against capsular polysaccharide antigens of S.pneumoniae, specifically it contains the protective epitopes of PspA. The protein can also be used in solid-phase immunoadsorbent assays, since it is readily bound to supports coated with monosialoganglioside GMI. The fusion protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae strain Rx1; pspA; immunoprotective; immunogen; pneumococcal surface protein A; cholera toxin B subunit; fusion protein;
subjects before surgery or insertion of an in-dwelling device (alternatively the device itself is impregnated before placement). The nucleic acid sequence is used as sources of antisense sequences (for therapeutic use) or regulatory elements for controlling expression of bacterial genes, and for antibacterial screening. The protein can be also used as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents an N-terminal peptide of pneumococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Truncated pneumococcal surface protein and cholera toxin B sub-unit fusion protein - useful as an immunogen against Streptococcus pneumoniae
                                                                                                                                                                                                                    ö
                                                                                                                                                                               Length 44;
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                                                                                                                                                                           100.0%; Score 23; DB 19;
llarity 100.0%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 0;
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91US-0656773.
93US-0072065.
95US-0469434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW71314 and AAW79337-39 represent Staphylococcus aureus WCHU (NCIMB 4071) proteins that have homology to Haemophilus influenzae haein lipoic acid synthetase (lipoate biosynthesis protein A (lipA) homologue. The protein is used to generate antibodies and to screen for antimicrobials. The products are used to treat or prevent bacterial infections, particularly where caused by S. aureus but also against Helicobacter pylori. Particular applications are to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid from Staphylococcus aureus NCIMB 40771 - useful for, e.g. diagnosis, prevention and treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae; haein lipoic acid synthetase;
lipoate biosynthesis protein A; lipA; treatment; prevention;
bacterial infection; Helicobacter pylori; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 21; Length 41; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus haein lipoic acid synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW79339 standard; Protein; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Pages 51; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                               99US-0161406.
99US-0161359.
99US-0161360.
                                                                                                                                                                                                                                                                                                            99US-0161992.
99US-0161993.
99US-0162142.
                                        99US-0160768
99US-0160770
                                                                              99US-0160814
99US-0160815
                                                                                                                     99US-0160980.
99US-0160981.
                                                                                                                                                           99US-0160989
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                                                                                                                                                                           99US-0161404
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                                                                                                                                                                                                                                                                          99US-0161361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                99us-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-322718/28.
                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV59884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9823738-A2
                                                                            21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYDA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection(s)
                                        21-0CT-1999;
21-0CT-1999;
                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                           25-OCT-1999;
25-OCT-1999;
                                                                                                                                                                                                                    25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-1998
                                                                                                                                                                                                                                    26-0CT-1999
                                                                                                                                                                                                                                                        26-OCT-1999
                                                                                                                                                                                                                                                                          26-OCT-1999
                                                                                                                                                                                                                                                                                            28-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warren RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW79339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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pat943-1.rag

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pneumoniae

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PspA; pneumococcal surface protein A; immunoprotection; detection; GMI; solid phase immunosorbent assay; epitope; cell membrane anchor region; cholera toxin B subunit; CTB; monosialoganglioside; fusion protein.

    S. pneumoniae truncated pspA protein fragment #1.

                              AAW92457 standard; Protein; 45
                                                                                                                                                                 Streptococcus
                                                                          21-APR-1999
                                                                                                                                                                                      US5871943-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DYDA 4
                                                                                                                                                                                                                                                                                                                                    Briles DE,
                                                    AAW92457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 18
AAW04953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                   AAW9245
                               Pp
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                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoprotective pneumococcal surface protein A (PSpA) N-terminal sequence. The present invention also describes a method of forming the immunoprotective truncated PspA, comprising incorporating a vector bacterium via transformation. (I) is used to design primers which are capable of detecting a large number of S. pneumoniae strains, which in turn can be used to diagnose pneumococcal infection in mammals (e.g. humans), independent of the strain which has caused it. The PspA protein is used to develop a vaccine against pneumococcal infection comprising, as an immunologically active component, a live attenuated or killed bacteria containing a gene coding for the truncated form of PspA.
                                                                                   Gaps
more immunogenic against S.pneumoniae than using PspA alone as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a truncated pneumococcal surface protein A used in development of pneumococcal infections -
                                                                                  ;
0
                                                                                                                                                                                                                                                                    Streptococcus pneumoniae Rx1; PspA; immunoprotective; vaccine; diagnosis; infection; pneumococcal surface protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a Streptococcus pneumoniae Rx1
                                                           Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 45;
                                                                                Indels
                                                                                                                                                                                                                                               Streptococcus pneumoniae Rx1 PspA N-terminal sequence #1.
                                                                     2.2e+02;
hes 0;
                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 20;
Pred. No. 2.2e+02;
Mismatches 0;
                                                        Score 23; DB
Pred. No. 2.2¢
; 'Mismatches
                                                                                                                                                                             AAY41839 standard; Protein; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 27pp; English
                                                                             0;
                                                        100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                          92US-0835698.
91US-0656773.
                                                                                                                                                                                                                                                                                                                                                                      94US-0247491.
                                                                                                                                                                                                                           (first entry)
                                                                              Conservative
                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                           (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Briles DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-579913/49.
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                  45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 AA;
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|DYDA 17
                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1994;
                                                                                                                                                                                                                          08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-1992;
15-FEB-1991;
                                                                                                  1 DYDA 4
                                                                                                                                                                                                                                                                                                                                               12-OCT-1999.
                                                                              4
                                                                                                                                                                                                                                                                                                                          US5965400-A
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yother JL,
             immunogen.
                                  Sequence
                                                                                                                                                                                                    AAY41839;
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                                                                                                                        14
                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a fragment of the truncated form of the Streptococcus pneumoniae PspA protein which is used in a solid phase immunosorbent assay for detecting a PspA (pneumococcal surface protein A) antibody and antigen. This truncated protein contains the antibody and antigen of the complete protein contains the excludes the cell-membrane anchor region) fused to the B subunit of cholera toxin (CTB) which is bound to monosialogangloside (GMI) coated on the substrate. The use of a fusion between truncated PspA and cholera toxin B subunit (CTB) allows the support to be coated without having to isolate PspA fragments since CTB binds specifically to the GMI coating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cellulytic enzyme; endoglucanase; hydrolysis; cellulose; microorganism; plant cellulase; catalytic region; textile; backstaining; bio-polishing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                           Immunosorbent assay for pneumococcal surface protein A antigen or antibody - for diagnosis of infection by Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 20;
Pred. No. 2.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Partial D. gossypina endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 24pp; English.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW04953 standard; peptide; 49
                                                                                    92US-0835698.
91US-0656773.
93US-0072068.
95US-0468718.
                                           95US-0468718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                           Yother JL;
                                                                                                                                                                                                (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                  WPI; 1999-166635/14.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the solid support
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 AA;
                                                                                    12-FEB-1992;
15-FEB-1991;
                                         06-JUN-1995;
                                                                                                                             03-JUN-1993;
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16-FEB-1999
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Gaps

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Indels

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Conservative

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DYDA 4

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AAW04938-W04963 represent partial endoglucanase sequences. These peptides are examples of fragments of the enzymes of the invention (see AAW04925 for an example of a full length enzyme of the invention). The full length enzyme of the invention). The full length enzymes possess cellulytic (particularly endoglucanase) activity. Cellulytic enzymes are involved in the hydrolysis of cellulose, and are synthesised by a large number of microorganisms and plants. The enzymes of the invention containing the conserved catalytic regions (such as AAW04913) exhibit improved performance, e.g. 50 times higher performance, compared to multiple domain enzymes. The enzymes can be used for the treatment of fabrics or textiles, preferably for preventing backstaining, for blo-polishing or for stone-washing cellulosic fabric. They can also be used for the degradation or modification of plant material, such as cell walls. They can also be used in the treatment of paper pulp preferably for debarking, defibration, fibre modification, enzymatic de-inking or drainage improvement.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin;
stone-washing; cellulosic fabric; colour clarification; defibration; cell wall degradation; paper pulp; debarking; fibre modification; enzymatic de-inking; drainage improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 New endo:glucanase enzyme preparations - contg. conserved catalytic regions, useful for treating fabrics, textiles, plant material or paper pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human apoptosis regulatory kinase homologue, SEQ ID NO:1476.
                                                                                                                                                                                                                                                                                                                                      Kauppinen MS, Lange L, Lassen SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 217; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                       Takagi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
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                                                                                                                                                                                                                     95DK-0000885.
95DK-0000886.
95DK-0000887.
                                                                                                                                                                                         96DK-0000137.
95DK-0000272.
                                                                                                                                                          96WO-DK00105
                                                                                                                                                                                                                                                                      95DK-0000888
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                                                                                                                                                                                                                                                                                                                                                    Nielsen RI, Schuelein M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                     Ihara M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-443173/44.
                                                               Diplodia gossypina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT39091
                                                                                                                                                                                                                                                                                                                                     Andersen LN,
                                                                                            WO9629397-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 DYDA 14
                                                                                                                                                          18-MAR-1996;
                                                                                                                            26-SEP-1996
                                                                                                                                                                                                        17-MAR-1995;
                                                                                                                                                                                                                       08-AUG-1995
                                                                                                                                                                                                                                                                       08-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYDA 4
                                                                                                                                                                                                                                                       08-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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sequences ABA08255-ABA09374 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence of the invention activities; the polypeptides of the invention may have various activities; stem cell growth factor activity; hammunomodulatory activity; tissue growth activity; hammunomodulatory activity; activit, tissue growth activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; ancer cell proliferation or metastasis.

Thrombolytic activities; ancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conduitions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), artherial isohaemia hone disorders (e.g., myeloid or lymphone), and almorated or corrected the activities of arthritis), artherial isohaemia hone disorders (e.g., myeloid or lymphone), and almorated e.g., and alm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reterial isotalemy, auneroscierosis, coronary neart disease, arterial isotalemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound haling (e.g., of burns, incisions and ulcers), while those with cimmunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelal cells that can be used to augment or replace cells damaged by illness, that can be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human to polypeptide of the invention.
inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; tumour asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; osteoporosis; vascular growth disorder; citissue regeneration; wound healing; infection; immune disorder; antiasthmatic; antiarthitic; heemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 146; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-2001; 2001WO-US03800
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N-PSDB; ABA08350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157188-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by construct and disorders include SAPHO Syndrome (synovitis, acne, pustulosis, hypertosis and osteomyclitis), uveitis and endophthalmitis. Practuosis, hypertosis and osteomyclitis), uveitis and the central carries associated with an infections of bone, joints and the central esions associated with acne vulgaries. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that plands to the proteins of the invention of sumple with a binding agent that pland protein in the sample. The polypeptides may be used as antigens in the production of antibodies of specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and convention and activity of P. acnes proteptides and diagnostic agents for determining P. acnes presence, for example, by carry in the sequence data for this patent did not form part of the printed car finked immunosorbent assay (ELISA).

Converse the sequence data for this patent did not form part of the printed at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; |joint, central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                               ;
                                                            Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia A;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes immunogenic protein #27954.
                                                     Score 23; DB 22;
Pred. No. 2.9e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham JL, Wang S
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID No 28253; 1069pp; English.
                                                                                                                                                                                                                                              AAU67058 standard; Protein; 61
                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes.
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                                                 Query Match
Best Local Similarity
                  58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS59776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181581-A2.
                                                                                                                                               DYDA 23
                                                                                                                                                                                                                                                                                                                    27-FEB-2002
                                                                                                                       1 DYDA 4
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                    Sequence
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                                                                                                                                                                                                                                                                                                    Duffy protein; DP; binding affinity; malarial Duffy-binding ligand; MDBL; human; gp-Fy-alpha; gp-Fy-beta; malaria; inhibit; invasion; red blood cell; malarial parasite; merozoite; Plasmodium vivax; P. knowlesi; treatment; regulation; erythrocyte; neural; renal function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a Duffy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides AAW62589-91 have amino acid sequences characteristic of a Duffprotein (DP) and specific binding affinity for malarial Duffy-binding ligand (MDBL). The human Duffy protein can be a gp-fy-alpha or a gp-fy-beta protein. The peptides are used to protect against malaria. They pecifically inhibit the invasion of red blood cells by malarial They pecifically inhibit the invasion of red blood cells by malarial The peptides can also be used to generate antibodies, complementary peptides and drugs modelled on their tertiary structures, and are all essentially useful in treatment of malaria and in the regulation of essential erythrocyte, neural and renal functions.
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide(s) from Duffy protein that bind to malarial Duffy binding ligand - used to protect against infection by malarial parasites, particularly plasmodium vivax or Plasmodium knowlesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·;
                                                                                                                                                                                                                                                                          Peptide having affinity for a malarial Duffy-binding ligand.
                                              Length 61;
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                                                                        Indels
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                                           Score 23; DB 22;
Pred. No. 3e+02;
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100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
                                                                      Mismatches
                                                                                                                                                                                         AAW62591 standard; peptide; 64 AA.
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                                        100.0%;
100.0%;
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                                                                                                                                                                                                                                                   (first entry)
                                                                    Conservative
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                                     Query Match
Best Local Similarity
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             61 AA;
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tes 4; Conserv
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                                                                                                                        46 DYDA 49
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1997;
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                                                                                              1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998.
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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             Sequence
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                                                                 Matches
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Matches
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RESULT

AAR73956;

AAR73956

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Peptides AAW62589-91 have amino acid sequences characteristic of a Duffy protein (DP) and specific binding affinity for malarial Duffy-binding ligand (MDBL). The human Duffy protein can be a gp-Fy-alpha or a gp-Fy-beta protein. The peptides are used to protect against malaria. They pecifically inhibit the invasion of red blood cells by malarial parasites, specifically merozoites of Plasmodium vivax and P. knowlesi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The peptides can also be used to generate antibodies, complementary peptides and drugs modelled on their tertiary structures, and are all potentially useful in treatment of malaria and in the regulation of essential erythrocyte, neural and renal functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       group; antigen; alpha; beta; cell; malaria; treatment.
                                                                                                                                                                                                                                                                                      New peptide(s) from Duffy protein that bind to malarial Duffy binding ligand - used to protect against infection by malarial parasites, particularly Plasmodium vivax or Plasmodium knowlesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding gp-Fy, Duffy antigen proteins - used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 19;
100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW54861 standard; Protein; 66 AA.
                                                                                                                                                                       (NYBL-) NEW YORK BLOOD CENT INC.
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                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 4; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gp-FY protein; Fyb71-81; duffy
alternative splicing; RBC; red
                                                                                            97WO-US21063.
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                                                                                                                                 96US-0749526
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                                                                                                                                                                                                             Pogo OA;
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Matches 4; Conserva
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42 DYDA 45
                  WO9821235-A1
                                                                                          14-NOV-1997;
                                                                                                                                 15-NOV-1996;
                                                                                                                                                                                                             Chaudhuri A,
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                                                    22-MAY-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding gpD protein component to Duffy blood group antigen - also proteins, peptide(s) and vaccines for the therapy of malaria, and the regulation of erythrocyte, neural and renal functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The N-terminal region of the gpD protein has been identified as being involved in the interaction of the malaria parasite with the red cell. This peptide binds the Rubinstein antibody which is a monoclonal antibody specific for the gpD protein. The fact that this peptide along with those of AAR73957-58 bind the Rubinstein antibody whereas AAR73959-61 do not suggest that the junction between the C-terminal of peptide AAR73951 and the N-terminal of AAR73959 is important for binding. This peptide binds the parasite in vivo and, therefore, can be used as the immunogen in a vaccine against malaria.
                                                                                                                                                                 Duffy blood group; malaria; Plasmodium vivax; glycoprotein; gpD; cytokine receptor.
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                                                                                                                               Duffy blood group gpD protein antigen N-terminal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 16;
100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
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              AAR73956 standard; Peptide; 66 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                           (NYBL-) NEW YORK BLOOD CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pogo A;
                                                                                                                                                                                                                                                                                                                                                 94WO-US12028
                                                                                                                                                                                                                                                                                                                                                                                     93US-0140797
                                                                                          (first entry)
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Matches 4; Conserv
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DYDA 45
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                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                               20-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-1993;
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                                                                                        22-NOV-1995
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Sequence

Query Match

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RESULT 23

Synthetic

AAW62590;

AAW62590
11D AAW6
12D AAW6
12D AAW6
12D 17-S
12D 17-S
12D PEPT
12D PET
12D PE

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Gaps

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Length 66; Indels

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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immobilized multi-enzyme complex, optionally modified, and a method
prevent vivax malaria and to regulate erythrocyte, neural or renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium; multienzyme complex; immobilised body; carrier; food; cohensin-dockerin; cellulose bound protein; medicine.
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                                                                                                                                             complementary peptides and drugs
                                                                         The sequence is that of a peptide which specifically binds the anti-Fy6 antibody, which blocks penetration of P.vivax merozoites into human erythrocytes in vitro. The peptide may thus be useful in preventing malaria and may also be modelled on its tertiary structure.
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                                                                                                                                                                                                                         Length 66;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium thermocellum amino acid sequence SEQ ID NO:8
                                                                                                                                                                                                                      100.0%; Score 23; DB 19;
100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 10; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                 AAB12795 standard; protein; 67 AA
                                            Claim 10; Page 13; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                     Query Match
Best Local Similarity
A; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its preparation
                                                                                                                                                                                          66 AA;
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42 DYDA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB12795;
                                                                                                                                                                                          Sequence
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                function
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polymeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PECR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PECR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymetide are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating tisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGO0010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 22;
100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #23856.
                                                                                                                                                                                                                           ABG23865 standard; Protein; 68 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
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2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS88052
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23-AUG-2000;
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63 DYDA 66
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Best Local Similarity 100.0%; Matches 4; Conservative (

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA2135). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 35743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                 Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
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ilarity 100.0%; Pred. No. 3.5e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID No 27816; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                          ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
                                                                                                                                                                                                                                                                             30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                      congenital heart disease.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 AA;
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                                                                                                                             WO200157274-A2
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                                                                                             Homo sapiens.
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26-MAY-2000;
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34 DYDA 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe.
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0
                                                                                                                                                                                                                       Peptide #10253 encoded by human foetal liver single exon probe.
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                        ABB42747 standard; Peptide; 69 AA
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2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                  (first entry)
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                     WO200157277-A2.
1111
55 DYDA 58
                                                                                                                                                                                                                                                                                                Homo sapiens.
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27-SEP-2000;
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34 DYDA 37
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ABB26046
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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                 Rank
                                                                                                                                                                                                                                                                                                             AAM36561 standard; Protein; 69 AA.
                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                 gene expression in
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                                                       genome-derived single
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359
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                 Hanzel DK,
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                                   WPI; 2001-488900/53.
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                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                             69 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157272-A2
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21-SEP-2000;
27-SEP-2000;
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34 DYDA 37
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                                                                  analyzing
              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing
                                                                                                                                                                             Sequence
                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                              Probe;
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                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                             for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe;
                                                                                                                                                                                                                          650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 Length 69;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 22;
100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM76452 standard; Protein; 69 AA.
                                                                                                                                                                                           Single exon nucleic acid probes
                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                20000S-0180312.
2000US-0207456.
2000US-0608408.
2000US-0532366.
2000US-0234687.
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2000US-0608408.
2000US-0632366.
                             30-JAN-2001; 2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                    Hanzel DK,
                                                                                                                                                                       WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                            69 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157276-A2.
                                                          26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                             04-OCT-2000;
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                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM76452;
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Matches
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #10598 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                  acid probes useful for
                                                                                                                                                                                         Example 4; SEQ ID NO: 36758; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                   The present invention provides a number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 22; 100.0%; Pred. No. 3.5e+02;
                                                                                                               exon nucleic acid
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DR;
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JP63071180-A.
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                                                                                                                                                                                                                                              Human peptide encoded by genome-derived single exon probe SEQ ID 35381.
                                                                                                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicotycsis; lymphangloleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary ciliary dyskinesis; pulmonary hypertension;
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                                                                      Gaps
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0
                                               Length 69;
                                                                      Indels
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0
                                              100.0%; Score 23; DB 22;
100.0%; Pred. No. 3.5e+02;
                                                                     Mismatches
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                                                                                                                                                                          ABG45716 standard; Peptide; 69 AA.
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2000US-0608408.
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2000US-236359P.
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hyaline membrane disease.
                                                                     4; Conservative
human genetic disorders.
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                                                          Best Local Similarity
                        69 AA;
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21-SEP-2000;
27-SEP-2000;
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34 DYDA 37
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                        Sequence
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                                                                      Matches
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or the eukarypote; and (D) desecting specific hypothesation of desectably labeled nucleic acids from eukarypote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon in several microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene or probes/open reading frames (ORP). The probes are used for gene or south as asthman lung derived mRNA and for the study of lung diseases such as asthma, lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary intensitial lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary hamonary alveolar proteinosis, karagener syndrome, sarcoidosis, pulmonary disease, bulmonary displasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein or encoded by a single exon probe of the invention. ö (b) detecting specific hybridisation of detectably Trigonopsis variabilis D-amino oxidase; Trigonopsis variabilis CBS 4095; high yields of D-amino acid oxidase; enzyme. Sequence encoded by of Trigonopsis variabilis D-amino acid oxidase gene, Using the DNA, (AAN81684) D-aminoacid oxidase (D-AO)can be prepd. in a Gaps D-amino acid oxidase (I) gene - derived from Trigonopsis variabilis ö Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Length 69; Indels 100.0%; Score 23; DB 23; 100.0%; Pred. No. 3.5e+02; Disclosure; Fig 2, pages 551; 12pp; Japanese. 0; Mismatches ftp.wipo.int/pub/published_pct_sequences. Ą Trigonopsis variabilis CBS 4095. AAP81871 standard; protein; 70 (ASAH) ASAHI CHEMICAL IND KK 86JP-0215878. 86JP-0215878. (first entry) Conservative WPI; 1988-128942/19. Query Match Best Local Similarity 69 AA; N-PSDB; AAN81684

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99US-0134768.
99US-0134941.
99US-0135124.
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18-JUN-1999;
18-JUN-1999;
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22-JUN-1999;
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                       high yield. A wide range of applications is possible. The whole DNA was extd. from T. variabilis CBS 4095 by Cryer's method. 40 ug of the DNA C state. Its reacted with 4 units of the restriction enzyme MboI at 37 degrees C for 15 min. The reaction liquor is extracted with phenol./Chloroform C electrophoresis and electro-elution and dissolved in 20 ul of 0.1 fold concn. of TE buffer soln. (III) to give a soln. (IV). 30 ug of Vector C c nord. of TE buffer soln. (III) to give a soln. (V). (IV) and (V) c nord. If of 0.0 concn. of (III) to give a soln. (V). (IV) and (V) c nord. The vector and CBS 4095. A bNA library is prepd. The c are mixed in a ratio of 3:1 and reacted with T4-DNA ligase to combine the c mino gp. terminal AA sequence of D-AO is determined. A DNA probe is synthesized. Candidates of the D-AO-clone are selected and sepd. from the C synthesized. Candidates of the D-AO-clone are selected and sepd. from the c determined. D-AO gene is modified. A generation vector is prepd. and the C D-AO gene is smodified. A generation vector is prepd. and the C D-AO gene is generated. D-MELIA in the continual continual in the continual 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                   h 100.0%; Score 23; DB 9; Length 70; Similarity 100.0%; Pred. NO. 3.5e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 9363.
                                                                                                                                                                                                               gene is generated. D-methionin
E.coli contg. the recombinant.
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9905-0123548.
9905-0125788.
9905-0125786.
9905-0126785.
9905-0128234.
9905-012845.
9905-013047.
9905-0130891.
9905-0130891.
9905-0130891.
9905-0131449.
9905-0132484.
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Matches 4; Conserv
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54 DYDA 57
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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28-APR-1999;
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25-FEB-2000; 2000EP-0301439
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05 - MAR - 1999;

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10 - APR - 1999;

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99US-0147192.
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99US-0151438.
99US-0151930.
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99US-0160814.
99US-0160815.
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99US-0160741
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                             Length 70;
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                                                                                                                                                                                          Score 23; DB 21;
Pred. No. 3.5e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           AAG54077 standard; Protein; 70 AA.
                                                                                                                                                                                           100.0%;
.larity 100.0%;
Conservative 0;
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9905-0161404-
9905-0161405-
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9905-0161359-
9905-0161360-
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   99US-0160981
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Best Local Similarity
Matches 4; Conserv
22-0CT-1999;
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57 DYDA 60
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2000US-0246475.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
                                                                                                                                                                                    Gaps
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                                                                                                                                      Length 70;
                                                                                                                                                                                  Indels
                                                                                                                                 100.0%; Score 23; DB 21;
llarity 100.0%; Pred. No. 3.5e+02;
Conservative 0; Mismatches 0;
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14-AUG-2000; 2000US-0225759.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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2000US-0227009
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                                                                                                                                                           Local Similarity
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|DYDA 60
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28-0CT-1999;
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23-AUG-2000;
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ABB 5902

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20000S-0199076
20000S-0198123
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2000US-0225213.
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2000US-0225267
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2000US-0225270
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2000US-0225757
2000US-0225759
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2000US-0226681.
2000US-0226868.
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2000US-0231968.
2000US-0232397.
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2000US-0229344.
2000US-0229345.
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2000US-0228924
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2000US-0231242
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2000US-0229513
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26-JUL-2000;
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14-AUG-2000;
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18-AUG-2000;
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06-SEP-2000;
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                                                  02-AUG-2001
           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the traptiment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human reproductive system related antigen SEQ ID NO: 3861.
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17-NOV-2000; 2000US-0249211.
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                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2001; 2001US-0259678
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Matches 4; Conservative
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DYDA 11
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2001US-0259678
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(HUMA-) HUMAN GENOME SCI INC

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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
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N.B. The sequence data for this patent did not form part of the printed uspecification, but was obtained in electronic format directly from the USPIO web site.
                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human reproductive system related antiyens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                       Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3420.
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                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 3861; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 22; Length 79; llarity 100.0%; Pred. No. 4e+02; Conservative 0; Mismatches 0; Indels
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   Ruben SM;
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97US-064964P.
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Barash SC,
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Best Local Similarity
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                                                                                          N-PSDB; AAL01173
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08-NOV-1997;
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8 DYDA 11
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Rosen CA,
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ABP 38575
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 21383.
                                                          AAG19542 standard; Protein; 81 AA.
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99US-0123548.
99US-0125788.
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99US-0135124.
99US-0135353.
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99US-0134370.
99US-0134768.
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990S-0139119.
990S-0139453.
990S-0139453.
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990S-0137222.
990S-0137528.
990S-0137502.
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99US-0138094.
99US-0138540.
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99US-0130510
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99US-0132484
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99US-0132486
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99US-0134256
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99US-0136392.
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                                                                                                       (first entry)
                                                                                                                                                                                            Arabidopsis thaliana
     41 DYDA 44
                                                                                                      17-OCT-2000
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04-MAY-1999;
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                                   RESULT 4(
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                                                         ö
                                                                                                                                                                                                                                          Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a H. pylori transporter protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypetide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from DNA. The sequences were analysed for ORP of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To indentify likely H. pylori antigenes for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant and determined the sequences of interest, particular regions can be production to the pylori by pcR miplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid'sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                         ;
0
                               100.0%; Score 23; DB 23; Length 79; 100.0%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 18; Length 81; 100.0%; Pred. No. 4.1e+02; ative 0; Mismatches 0; Indels
                                                        0; Indels
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                                                                                                                                                                                                                     H. pylori transporter protein 289711.aa.
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                                                                                                                                                    AAW20370 standard; Protein; 81 AA
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95US-0487032.
                                                                                                                                                                                               14-JUL-1997 (first entry)
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-052306/05.
N-PSDB; AAT67562.
                                                                                                                                                                                                                                                                                      Helicobacter pylori
                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
          79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 AA;
                                                                                       1111
47 DYDA 50
                                                                                                                                                                                                                                                                                                          WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                       06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                           01-APR-1996;
07-JUN-1995;
                                                      4;
                                                                           1 DYDA 4
                                                                                                                                                                                                                                                                                                                                  19-DEC-1996.
                                                                                                                                                                           AAW20370;
          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                     Matches
                                                                                                                                 RESULT 39
                                                                                                                                            AAW20370
                                                                                                                                                               XX
SO
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18-JUN-1999; 18-JUN-1999;

0;

Gaps

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Conservative

Matches

DYDA 4

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Score 23; DB 21;
Pred. No. 4.1e+02;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
   990S - 0149426
990S - 0149723
990S - 0149929
990S - 0149929
990S - 0149929
990S - 0149929
990S - 015966
990S - 0151065
990S - 0151065
990S - 0151080
990S - 0161090
990S - 0161090
990S - 01611360
990S - 01611360
990S - 01611360
990S - 01611360
   18 - AUG - 1999;
20 - AUG - 1999;
20 - AUG - 1999;
23 - AUG - 1999;
25 - AUG - 1999;
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15.SEP-1999;
16.SEP-1999;
20.SEP-1999;
23.SEP-1999;
24.SEP-1999;
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05-0CT-1999

06-0CT-1999

13-0CT-1999

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||DYDA 13
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ABG26683
ID ABG26
XX
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       δλ
 990S-0139456.
990S-0139457.
990S-0139458.
990S-0139460.
990S-0139461.
990S-0139463.
990S-0139750.
990S-0139789.
990S-0139817.
990S-0139817.
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990S-0145919
990S-0145919
990S-0146386
990S-0146388
990S-0147038
990S-0147204
990S-0147192
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99US-0140991.
99US-0141287.
99US-0141842.
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990S-0142390.
990S-0142390.
990S-0142803.
990S-0142977.
990S-0143542.
990S-0144085.
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990S-0144632
990S-0144814
990S-0145086
990S-0145086
990S-0145087
990S-0145087
990S-0145192
990S-0145192
990S-0145192
990S-0145165
990S-0145165
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99US-0147416.
99US-0147493.
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99US-0148171.
99US-0148319.
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99US-0148684.
99US-0149368.
99US-0149175.
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99US-0144334.
99US-0144335.
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99US-0144331.
99US-0144332.
18 - JUN - 1999;

23 - JUN - 1999;

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29 - JUL - 1999;

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21 - JUL - 1
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15 - 70L - 1999;
16 - 70L - 1999;
19 - 70L - 1999;
20 - 70L - 1999;
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21 - 70L - 1999;
22 - 70L - 1999;
22 - 70L - 1999;
23 - 70L - 1999;
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23 - 70L - 1999;
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28 - JUL - 1999
02 - AUG - 1999
03 - AUG - 1999
04 - AUG - 1999
05 - AUG - 1999
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11 - AUG - 1999
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13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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Gaps

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Length 81; Indels

Homo sapiens

11-0CT-2001

31-MAR-2000; 23-AUG-2000;

biodiversity

A COURT COUR

Claim

18-FEB-2002

ABG26683;

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"X represents a gap in the sequence corresponding to residues 146-155 when in alignment with BASBPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= unknown
/note= "X represents a gap in the sequence corresponding
to residues 173-188 when in alignment with BASBPN'
                                                                   Subtilase; variant; mutant; subtilisin; serine protease; Bacillus sp.; auto-proteolytic stability; laundry; dishwashing; proteolytic activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New subtilase variants with increased auto-proteolytic stability and related nucleic acid, vectors and transformed cells - useful in laundry and dishwashing compositions, having increased proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New subtilase enzyme variants have been derived from a precursor subtilase having either (i) an autoproteolytic cleavage site between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Von
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "X represents
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                  'label= unspecified
                                                                                                                                                                                                                                                     label= unspecified
                                                                                                                                                                                                                                                                                       label= unspecified
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                                                                                                                                                                                                                                                                                                                                                                                                label= unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= unspecified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97DK-0000284.
96DK-0001235.
96DK-0001240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-DK00500
                                                                                                                                            Staphylococcus epidermidis.
(first entry)
                                   Subtilase SEEPIP fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bauditz P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-286932/25
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 23-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-1997;
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05-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen C,
                                                                                                           detergent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, oplymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The chair first and in recombinant production of (II). The chair if the consistence of the fidentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II), (I) and (II) are useful in medical in gene in protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human crown and part of the sequence of the invention.

CNOTE: The sequence data for this patent did not appear in the printed sequences.

Specification, but was obtained in electronic format directly from WIPO control format the printed control of the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and 'encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 22;
Pred. No. 4.1e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; SEQ ID No 57042; 103pp; English.
                                                            Novel human diagnostic protein #26674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW62245 standard; protein; 84 AÅ
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0
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                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                 2000US-0540217
2000US-0649167
                            (first entry)
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N-PSDB; AAS90870.
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Best Local Similarity
'-has 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                 Human; chromosome
                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AA;
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Der Osten

||||| |DYDA 71

68

AAW62245

RESULT 42 AAW62245

1 DYDA 4

δλ

Sequence

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cc residues 132 and 133 (all numbering according to the subtilisin BPN sequence (BASBPN)) or (ii) at least 1 amino acid (aa) modification at positions corresponding to G159, S164, I165, V167, R170 or Y171 of BLS309, by substitution, insertion or deletion of at least 1 of the residues 129-136 so that autoproteolysis stability is increased, and the compositions together with a cellulase, lipse, cutinase, oxidoreductase, another protease or amylase. The other components are of shandard surfacterates, builders or bleaches. A typical granular fabric cleaning composition comprises 6.5% sodium 12C alkylbenzenesulphonate; 15% Na2 sulphate; 26% zeolite A; 5% Na nitrilotriacetate; 0.1% of the subtilase variant; 0.5% poly(vinyl-perborate monohydrate; 0.1% of the subtilase variant; 0.5% poly(vinyl-perborate monohydrate; 0.1% phenol sulphonate and minor components to make 100%. The subtilase variants are used in laundry and dishwashing detergents also in fabric softeners and hard-surface cleaners. Increased resistance to autoproteolysis results in greater proteolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardlovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 19; Length 84; 100.0%; Pred. No. 4.3e+02; ive 0; Mismatches 0; Indels'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX protein sequence SEQ ID NO:11406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP05712 standard; Protein; 86 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-106308/14.
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es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                               84 AA;
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DYDA 24
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Disclosure; SEQ ID 11406; 1037pp; English

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                                     Treferred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABM15762 to ABM2725 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple solerosis, rheumatoid as multiple sesses, autoimmune disorders such as multiple solerosis, rheumatoid as multiple solerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3. The sequence data for this patent did not form part of the printed ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; prepancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorthoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapphing; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                             arthritis, autoimmune thyroiditis, myasthenia gravis, ineumacoid disease and autoimmune inflammatory eye disease. ORFX profers see also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                   present invention describes substantially purified human proteins
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                                                                                                                                                                                    The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polypuncleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related of sorders. Such conditions include ovarian cancer and breast cancer, and clasorders (e.g., infertility, disorders of pregnancy, anovulation.) activation or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation.) and covarian or breast crimers, such on the production of clasorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., champing), cardiovascular disorders, and unimary system disorders, neurological disorders, gastrointestinal disorders, and unimary system disorders, ovarian antigen polypeptides and conditions (e.g., diamemia), cardiovascular disorders, and unimary system disorders, ovarian inscreening for compounds which further be used for gene therapy, chromosome mapping, in the printed that the covarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and and phenotyping. The printed sequence represents a human ovarian antigen of the invention.

Sequence represents a human ovarian antigen of the invention.

Sequence represents a human ovarian antigen of the invention.

Sequence represents a human ovarian antigen of the printed specification, but was obtained or sequences.
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                                                        Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
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Pred. No. 4.4e+02;
Mismatches 0;
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                                                                                                                                                     Claim 11; SEQ ID No 3483; 2922pp; English.
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tive 0;
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2002-147878/19.
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Best Local Similarity
WPI; 2002-147878,
N-PSDB; ABQ55428
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3-JUL-1999; 5-JUL-1999; 6-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 9-JUL-1999; 1-JUL-1999; 9-JUL-	2. July 1999; 2. July 1999; 3.	11-Aug-1999; 99 13-Aug-1999; 99 13-Aug-1999; 99 13-Aug-1999; 99 17-Aug-1999; 99 17-Aug-1999; 99 20-Aug-1999; 99 21-Aug-1999; 99 22-Aug-1999; 99 23-Aug-1999; 99
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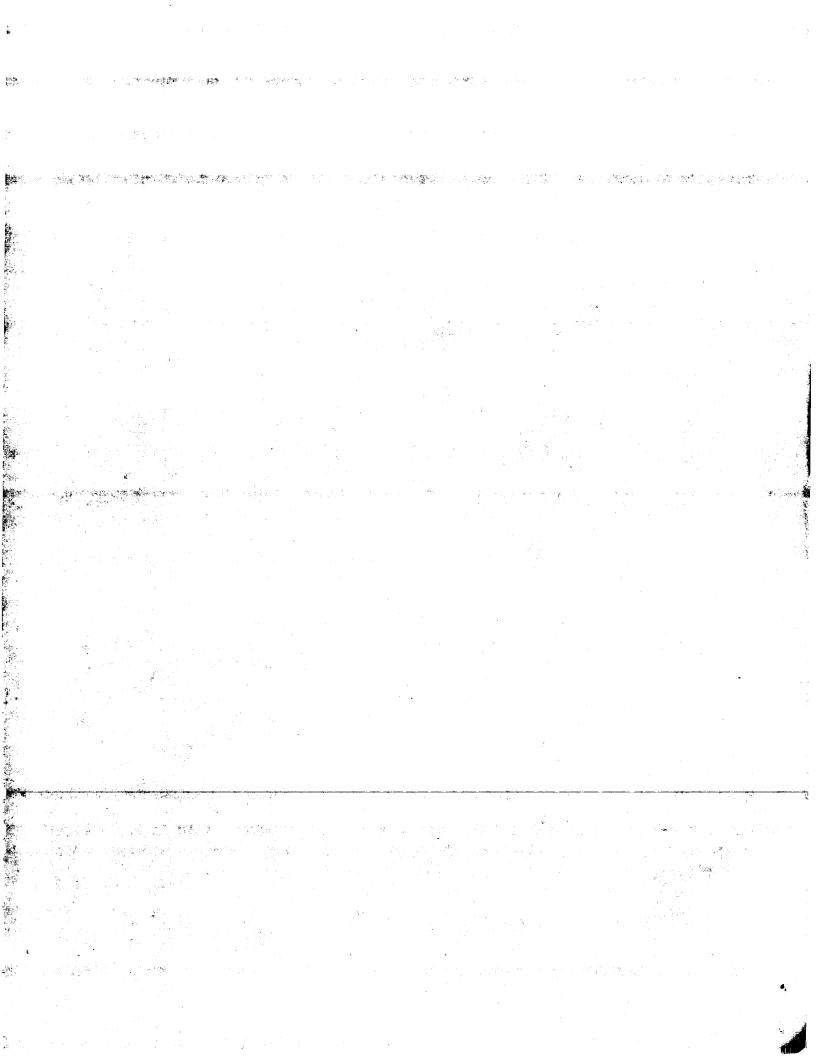
PR 04-OCT-1999; 99US-015773.
PR 05-OCT-1999; 99US-015773.
PR 05-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158239.
PR 13-OCT-1999; 99US-0158239.
PR 13-OCT-1999; 99US-0158239.
PR 14-OCT-1999; 99US-0159239.
PR 14-OCT-1999; 99US-0159231.
PR 14-OCT-1999; 99US-0159231.
PR 14-OCT-1999; 99US-015928.
PR 14-OCT-1999; 99US-015928.
PR 12-OCT-1999; 99US-0150767.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160780.
PR 22-OCT-1999; 99US-016081.
PR 22-OCT-1999; 99US-016130.
PR 22-OCT-1999; 99US-016130.
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PR 22-OCT-1999; 99US-016193.
PR 23-OCT-1999; 99US-016193.
PR 28-OCT-1999; 99US-016193.

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Gaps

Search completed: February 6, 2003, 11:19:35 Job time : 29.8333 secs



GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Pebruary 6, 2003, 11:16:04; Search time 9.3333 Seconds
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12.610 Million cell updates/sec Run on:

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1 dyda 4 Title: Perfect score: Sedneuce: Scoring table:

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Total number of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Database:

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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Patent No. 5268270	Sequence 313, App	313,	313,	4, AF	102,	104,	96	3, 1	'n	θ,	m	4	'n	4	ω,	ı,	154	S	58,	3, 4	8	ω,	7,	7,	, '
SUMMARIES	ID	US-08-442-884-4	5268270-6	-637-	US-08-871-355A-313		-392-	US-08-630-915A-102	-630-	US-08-630-915A-96	US-08-072-070-3	US-08-214-164-3	US-08-469-434-3	US-08-214-222-3	US-08-467-852A-4	US-08-468-718-3	US-08-247-491A-4	US-08-312-949-3	46-	US-09-314-268-154	US-08-651-136C-58	US-09-229-911A-58	49-	3-140-	US-08-486-670A-8	-241-	-08-820-91	US-08-749-526-2
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15, Appl 3420, App 7, Appli 10, Appli 5, Appli 5, Appli 5, Appli 53, Appli 609, App 192, Appl 92, Appli 92, Appli 4, Appli 4, Appli	4, Appli
Sednence Sed	Sequence
US-08-963-851-15 US-09-134-001C-3420 US-09-109-266-4 PCT-US95-07372-10 US-09-109-266-5 US-09-28-246-5 US-09-28-246-5 US-09-28-246-5 US-09-28-246-5 US-09-28-246-5 US-08-858-207A-509 US-08-861-395-1 US-08-877-7598-92 US-08-817-355A-92	US-08-469-434-4
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800011088888844444	4 4 5

ALIGNMENTS

RESULT 1 US-08-442-884-4 S. Sequence 4, Application US/08442884 : Patent No. 5637490		
; GENERAL INFORMATION: ; ADDITIONATE MITERIAL SAND of al		
	IDASE GENE	
; NUMBER OF SEQUENCES: 23		
CE ADDRESS:		
; AUDRESSEE: Wenderoth, Lind & Ponack . STREET. 805 Fifteenth Street N W #700	#700	
Washington	2	
STATE: D.C.		
COUNTRY: U.S.A.		
CLF: COUCS		
; COMPUTER READABLE FORM: : MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb		
R: IBM Compatible		
0,		
; SOFTWARE: Wordperfect 5.1		
2		
NUMBER: U		
; CLASSIFICATION: 435		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER:		
; FILING DATE:		
`		
~		
; REGISTRATION NUMBER: 33,367		
; REFERENCE/DOCKET NUMBER:		
; TELECOMMUNICATION INFORMATION:		
; TELEPHONE: 202-371-8850		
; TELEFAX:		
; TELEX:		
; INFORMATION FOR SEQ ID NO: 4:		
8		
Ħ		
; TYPE: amino acid		
; STRANDEDNESS: single		
3Y: lir		
TYPE: peptide		

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1 DYDA 4

Query Match 100.0%; Score 23; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 31; Matches 4; Conservative 0; Mismatches 0; Indels

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Gaps ő

US-08-442-884-4

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                                                          # APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johnnnes FILLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM; MEGATIVE HOST CELLS | CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/171,872 | FILING DATE: 01-JUL-1987 |
                                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible |
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1,0, Version #1.30
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                          DB 6;
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 313, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                           0; !Mismatches
                                                                                                                                                                                                                                                                                                      100.0%; Score 23; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: RPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 313:
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-637-759B-313
10 DYDA 13
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16 DYDA 19
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US-08-637-759B-313
                                                                                                                                                                                                                                                                                                                                                                        1 DYDA 4
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qq
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Gaps
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    100.0%; Score 23; DB 2; Length 24; 100.0%; Pred. No. 38; 0; Indels:ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 313, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMS 101 CON
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/871,355A FILING DATE: 09-JUN-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB95/02875 FILING DATE: 11-DEC-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                Sequence 313, Application US/08871355A Patent No. 6015669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 3039-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEFAX: (404) 873-8794
TELEFAX: (404) 873-8794
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
US-08-871-355A-313
                                                                                                                                                                                                            US-08-871-355A-313
                                                                                                                1111
19 DYDA 22
                                                                                    1 DYDA 4
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US-09-201-945-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Sequence 102, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 2; Length 28; ilarity 100.0%; Pred. No. 45; Conservative 0: Migmatata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
PCT/GB93/01821
FILING DATE: 26-AuG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9218185.8
FILING DATE: 26-AuG-1992
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/630,915A FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: (212) 669-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: USA
21P: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-392-816-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Recelling, Peter L.
APPLICANT: Lomako, Joseph
APPLICANT: Gleowar-Singh, Dave
APPLICANT: Singletary, George W.
APPLICANT: Whelan, William J.
APPLICANT: Whelen, William J.
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 23; DB 4; Length 24; Best Local Similarity 100.0%; Pred. No. 38; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,816
FILING DATE: 18-DEC-1995
STREET: 2800 One Atlantic Center STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street CITY: Atlanta Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPMS 101
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELEPOMMUNICATION INFORMATION:
TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08392816
Patent No. 5859333
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                               COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 DYDA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-201-945-313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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STRANDEDNESS:
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US-08-072-070-3
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STATE:
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                                                                                                                                                                    Sequence 104, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE 227
CORRESPONDENCE ADDRESS:
                            Gaps
                            ;
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                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
met FULNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 1101-174
                          ;
0
       Pred. No. 62;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPARKS, Andrew B.
HOFFMAN, No. 6309820h
KAY, Brian K.
FOWLKES, Dana M.
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TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
     100.0%;
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-630-915A-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
New York
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Best Local Similarity
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                                                                                                                                       RESULT 8
US-08-630-915A-104
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5 DYDA 8
                                                       1 DYDA 4
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DYDA 8
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McConnell, Stephen J.
PENTION: POLIZEETIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
VENTION: USING SAME
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                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: Yother, Janet L
APPLICANT: MCDANIel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/O72,070
FILING DATE: 19930603
                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                      J, Ve
J, WELS
03-APR-1996
1781: 536
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; Patent No. 5476929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: MISTOCK, S. LESILG
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-96
                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                      New York
New York
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Best Local Similarity
Matches 4; Conserv
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CITY: Arlington
STATE: Virginia
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Gaps
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                                  Indels
                                                                                                                                                                                                                                                                                        APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: Wother, Jaret S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,434
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100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZORO-12202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
OPPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) A15-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,065
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
                                                                                                                                                                                  RESULT 12
US-08-469-434-3
Sequence 3, Application US/08469434
Patent No. 5753463
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/08214222; Patent No. 5804193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 45 amino acids
                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
           Best Local Similarity
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                                                                                                  ||||
|14 DYDA 17
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                                                                           1 DYDA 4
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US-08-214-222-3
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                                  Matches
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Patent No. 5728387

GENERAL INFORMATION:
APPLICANT: BRILES, DAVID E.
APPLICANT: YOTHER, JANET L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 23; DB 1; Length 45; Best Local Similarity 100.0%; Pred. No. 75; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,164
FILING DATE: 17-MAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION UNBER: US/08/214,73
FILING DATE: 15-FEB-1991
CLASSIFICATION: 424
ATCORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W.
REGISTRATION NUMBER: 22,651,177
REGISTRATION NUMBER: 22,651,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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  CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
FILING DATE: 15-FEB-1991
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0810
TELEXX: LUKRAY WASHINGTON
TELEX: LUKRAY WASHINGTON
TELEX: LUKRAY WASHINGTON
TELEX: LUKRAY WASHINGTON
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 6102-137

REFERENCE/DOCKET NUMBER: 6102-137

TELEFAX: (703) 415-0813

TELEFAX: (703) 521-0813

TELEFAX: (703) 521-0813

TELEX: LUKPAT WASHINGTON

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                          LENGTH: 45 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 DYDA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-214-164-3
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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δλ g

Gaps

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Indels

Length 45;

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100.0%; Score 23; DB 2; Length 45; 100.0%; Pred. No. 75; tive 0; Mismatches 0; Indels
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APPLICANT: Briles, David E
APPLICANT: Vicher, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,718
                                                                                                                                                                                              ;
0
                                                                                                                                                     100.0%; Score 23; DB 2;
100.0%; Pred. No. 75;
ive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,068
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application US/08468718
; Patent No. 5871943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite 1203, 2001 Jeff.
CITY: Alington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 3:
                                                                              TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-467-852A-4
           SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                  Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
                                                TYPE: amino acid
STRANDEDNESS: n/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                              14 DYDA 17
                                                                                                                                                                                                                          1 DYDA 4
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                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-468-718-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08467852A
Patent No. 5856170
GENERAL INFORMATION:
APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
APPLICANT: MCDANIEL, Larry S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG ILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 1; Length 45; 100.0%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                   ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible |
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/467;852A
FLING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 Fifth Avenue
CITY: New York
                                                                                  COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFRENCE/CDOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.00
Conservative
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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14 DYDA 17
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US-08-467-852A-4
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Gaps

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APPLICANT: BRILES, David E.
APPLICANT: WU, Hong-Yin
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION OF
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA)
FILE REFERENCE: 454312-2018
CURRENT APPLICATION NUMBER: US/08/446,201B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Doorbar, John
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Length 45;
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Pred. No. 75;
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                                                                                                         454312-2049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1995-05-19
EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-05-20
EARLIER FILING DATE: 1994-05-20
EARLIER FILING DATE: 1994-05-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1995-03-12
EARLIER APPLICATION NUMBER: 07/656,773
EARLIER FILING DATE: 1991-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 154, Application US/09314268; Patent No. 6346377; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
US-08-446-201-1
; Sequence 1, Application US/08446201B
; Patent No. 6042838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-08-446-201-1
                                   ATTORNEY AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECHONE: (212) 840-3333
TELEPHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 3:SEQUENCE CHARACTERESTICS:
LENGTH: 45 aming acids
                                                                                                                                                                                                                                                                                                                                                                                100.0%;
  30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-08-312-949-3
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
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                     CLASSIFICATION:
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LENGTH: 45
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        Sequence 4, Application US/08247491A
Patent No. 5965400
GENERAL INFORMATION:
APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCES:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 23; DB 2; Length 45; Best Local Similarity 100.0%; Pred. No. 75; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NOMBER: US/08/247,491A FILING DATE: 23-JUN-1994 ATTORNEY ACCESSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
.SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08312949
Patent No. 6027734
GENERAL INFORMATION
APPLICANT: Briles, David E.
APPLICANT: Wu, Hong-Yin
TITLE OF INVENTION: MUCOSAL ADMINISTRATION OF
TITLE OF INVENTION: PNEUMOCOCCAL ANTIGENS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Curtis, Morris & Safford, P.C.
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                        ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-08-247-491A-4
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ADDRESSEE: No. 63876900 No. 6387690disk of No. 6387690th America, I. STREET: 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/229,911A
                                                                                                                                                                                                                                                                                                                                          Takagi, Shinobu
TITLE OF INVENTION: No. 6387690el Endoglucanases
NUMBER OF SEQUENCES: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: POGO, A OSCAT
APPLICANT: Chaudhuri, Asok
TITLE OF INVENTION: MALARIAL BINDING SITE ON DUFFY
TITLE OF INVENTION: BLOOD GROUP PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                   RESULT 21
US-09-229-911A-58
; Sequence 58, Application US/09229911A
; Patent No. 6387690
; GENERAL INFORMATION:
; APPLICANT: Schulein, Martin
; Andersen, Lassen, Soren F.
; Kauppinen, Markus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-229-911A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/651,136
FILING DATE: 21-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08749526
Patent No. 5911991
                                                                                                                                                                                                                                                                                     Lange, Lene
Nielsen, Ruby I.
Ihara, Michiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 49 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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Best Local Similarity
4; Conserve
                                                        11 DYDA 14
                     1 DYDA 4
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US-08-749-526-3
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CUMTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1:0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lange, Lene
APPLICANT: Nielsen, Ruby I.
APPLICANT: Thara, Michiko |
APPLICANT: Takagi, Shinobu |
TITLE OF INVENTION: NO. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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; TITLE OF INVENTION: VIRUSES

; FILE REFERENCE: 3789/80902

; CURRENT APPLICATION NUMBER: US/09/314,268

; CURRENT FILING DATE: 1999-03-19

; EARLIER APPLICATION NUMBER: 09/314,268

; NUMBER OF SEQ ID NOS: 179

; SEQ ID NO 154

; LENGTH: 47
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                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human papillomavirus type 60
US-09-314-268-154
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
US-08-651-136C-58
; Sequence 58, Application US/08651136C
; Patent No. 6001639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schulein, Martin
Andersen, Lene N.
Lassen, Soren F.
Kauppinen, Markus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 60016390 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHOND: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 49 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-651-136C-58
                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             1111
23 DYDA 26
                                                                                                                                                                                                                                                                                                                                            1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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Gaps

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Indels

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Sequence 8, Application US/08486670A
Patent No. 5683696
CENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: THE CLONING OF DUFFY BLOOD GROUP ANTIGEN NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer & Woods
STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                           Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALDELFORM:
MEDIEM REALDELFORM:
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0
SOFTWARE: Worderfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,670A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/140,797
FILING DATE: October 21, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: NYBC 265-KGB
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 23; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 4; Conservative 0; Mismatches 0;
NAME: Kurt G. Briscoe
REGIGSTRATION NUMBER: 33.141
REFERENCE/DOCKET NUMBER: NYBC 265-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPHONE: (914) 332-1844
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 amino acids
                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid;
; TOPOLOGY: linear
US-08-486-670A-8
                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-140-797-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111
42 DYDA 45
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Patent No. 5578714
GENERAL INFORMATION:
APPLICANT: POGO, Angel Oscar; Chaudhuri, Asok
TITLE OF INVENTION: THE CLONING OF DUFFY BLOOD GROUP ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer & Woods
STREE: 660 White Plains Road
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 2; Length 64; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: LBM compatible
OPERATING SYSTEM: MS.DOS
SOFTWARE: WordPerfect
CRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,526
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/140,797
FILING DATE: 21-CT-1993
CLASSIFICATION: 536
PRIOR PETCATION: 536
PRIOR DATE: 21-CT-1993
CLASSIFICATION: MUMBER: 454-12
FILING DATE: 21-CT-1993
CLASSIFICATION NUMBER: 454-12
FILING DATE: 0,Dea, Sean W.
REFERENCE/DOCKET UNMBER: 454-12
TELECOMMUNICATION INFORMATION:
TELEFRAX: (516) 822-3550
TELEFAX: (516) 822-3550
TELEFAX: CLARRETISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: NCA.
COUNTRY: USA.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette, 3.50 inch, 800 kb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: System 7.0
SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,797
FILING DATE: October 21, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                            ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 4; Conservative
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                             New York
: USA
                                                                                   CITY: Jericho
STATE: New YOR
                                                                                                                                 COUNTRY: US
ZIP: 11753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 DYDA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-749-526-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Gaps

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Length 66;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: POGO, A OSCAT
APPLICANT: Chaudhuri, Asok
TITLE OF INVENTION: MALABIAL BINDING SITE ON DUFFY
TITLE OF INVENTION: BLOOD GROUP PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 2; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
TELERAX: 201 343-1684
TELERX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                             .отавек: US/08/850,917
02-MAY-1997
N. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 454-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/140,797
FILING DATE: 21-0CT-1993
CLASSIFICATION: 536
ATTORNEY,AGENT INFORMATION:
NAME: 0'Dea, Sean W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08749526 Patent No. 5911991
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                                                                                                                                                                                                                                                                                                                                                                                                                 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                        APPLICATION NUMBER:
FILING DATE: 02-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
US-08-850-917-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
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US-08-749-526-2
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                 Sequence 7, Application US/08241853
Patent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 1; Length 66; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
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Patent No. 5854045
Patent No. 5854045
PAPPLICANT: Pang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo |
TITLE OF INVENTION: ATTANSMEMBRANE TYROSINE PHOSPHATASE TITLE OF INVENTION: AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: ADDRESSE: ALBUBE & Jackson
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241/853
FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600-1-078
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION .....
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
TELEX: 133521
INFORMATION FOR ESQ ID NO: 7:
SEQUENCE CHRACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson.
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 66 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
US-08-241-853-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                  07601
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US-08-241-853-7
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Patent No. 597011
SERERAL INFORMATION:
APPLICANT: Weng, Zude
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Mied, Guo-Hua
APPLICANT: Mied, Guo-Hua
APPLICANT: Mied, Hajime
TITLE OF INVENTION: Plant Cell Proliferation-Associated Proteins
FILE REFERENCE: BB-1275-P1
CURRENT APPLICANTION NUMBER: US/09/109,266
CURRENT PILIG DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; Length 83;
Pred. No. 1.4e+02;
Mismatches 0; Indels
                                                                                                                                                                                    Sequence 7, Application US/08096741

Sequence 7, Application US/08096741

Settent No. 545374

GENERAL INFORMATION:

APPLICANT: Furuya, Kaoru

APPLICANT: Matsuda, Akio

TITLE OF INVENTION: A Transformant Capable of Producing
TITLE OF INVENTION: A Transformant Capable of NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSE: ADDRESS:

STREET: 1155 Avenue of the Americas
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/096,741
FILING DATE: 23-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INPORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 408-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9090
TELEFA: 6141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 amino acids
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York STATE: New York
                                                                            47 DYDA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||
62 DYDA 65
          4;
                                                 1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DYDA 4
                                                                                                                                                     RESULT 30
US-08-096-741-7
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          Matches
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: GTC-07

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-01-08

PRIOR FILING DATE: 1997-08-14

SEQ ID NO 3420

LENGTH: 79

WARDER TO A 3420

LENGTH: 79
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                                                                                                                                                                                          Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 4; Length 79;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: HANSEN, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVEWTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-048
CURRENT APPLICATION NUMBER: US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 68
                                                                                                                                                                                          100.0%; Score 23; DB 2; I 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3420, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-3420
                                                                                                                                                                                                                                                                                                                                                                                                US-08-963-851-15
; Sequence 15, Application US/08963851
; Patent No. 6300116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus epidermis
US-08-963-851-15
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100.0%;
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                    Conservative
                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-749-526-2
                                                                                                                                                                     Ouery Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  42 DYDA 45
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GENERAL INFORMATION:

APPLICANT: Staskawicz, B. S. et al.
APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Compositions
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
CURRENT APPLICATION NUMBER: 08/09/228,246
CURRENT APPLICATION NUMBER: 08/60,327
EARLIER FILING DATE: 1999-01-11
EARLIER FILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 5
SOSTHANE: PATENTING DATE: 1994-04-13
SOSTHANE: PATENTING DATE: 1994-04-13
SOSTHANE: PATENTING DATE: 1994-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
FILE REPERENCE: D6192CTP
CURRENT APPLICATION UNBER: US/09/518,046
EARLIER FILING DATE: 2000-03-02
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 4; Length 149; llarity 100.0%; Pred. No. 2.7e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: DOMAIN
; OTHER INFORMATION: protease domain of protease M (ProM)
US-09-518-046-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 4; L. Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                    ; Sequence 5, Application US/09228246
; Patent No. 6245510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 20, Application US/09518046
; Patent No. 6294663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 35
US-09-261-416-5
; Sequence 5, Application US/09261416A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Lycopersicon esculentum US-09-228-246-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
'-has 4; Conserve
                         122 DYDA 125
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LENGTH: 143
TYPE: PRT
                                                                                       RESULT 33
US-09-228-246-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DYDA 4
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LENGTH: 149
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                                                                                                                                                                                                                0;
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                                                                                                                                                                    Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 23; DB 5; Length 139; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Gln at position 20 starts
mature peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oklahoma Medical Research Foundation TITLE OF INVENTION: Calcium Binding Recombinant TITLE OF INVENTION: Antibody Against Protein C NUMBER OF SEQUENCES: 12 CORRESPONDENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: Patrea L. Pabst STREET: 2800 One Atlantic Center STREET: Alanta Atlanta Atlanta STREET: Alanta STREET: Atlanta STREET: Georgia
                                                                                                                                                         100.0%; Score 23; DB 2; L
100.0%; Pred. No. 1.8e+02;
.lve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: INC. Compatible | OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #11.0, Version #1.25 CURRENT APPLICATION NUMBER: PCT/US95/07372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PabSt, Datred 1, 284
REGISTRATION NUMBER: 31, 284
REFERENCE/DOCKET NUMBER: OMRF106CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 4
LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application PC/TUS9507372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: ...
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 20.139
OTHER INFORMATION:
OTHER INFORMATION:
                                                                    ; TYPE: PRT
; ORGANISM: Zea mays
US-09-109-266-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: I
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                       42 DYDA 45
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                                                                                                                                                                                                                                              1 DYDA 4
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Length 143;

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Gaps

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Sequence 1, Application US/08361395; Patent No. 5733768; GENERAL INFORMATION:
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 No. 6348328e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
; MOLECULE TYPE:
US-08-858-207A-509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
                                                                                                                                                       12 DYDA 15
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                                                                                                                               1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-361-395-1
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0
             GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TAGE-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
CURRENT PILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                     Serine protease catalytic domain of protease M (Prom) homologous to similar domain in TADG-12.
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 23; DB 4; Length 154; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: US-09-MAY-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 509, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PSTELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gimmi, Edward R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA ZIP: 19406-0939 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                 CTHER INFORMATION:
CTHER INFORMATION:
US-09-261-416-5
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
Patent No. 6291663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-858-207A-509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΡĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 DYDA 54
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                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 154
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER KEADABLE FURE:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Nelease #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAMM: EVANS, JOSEPh D.
REGISTRATION NUMBER: 148/42448
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8844
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
  Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 171;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                              APPLICANT: WRENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
Score 23; DB 4;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 2;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                            0; Mismatches
                                                                                                                                                                                                    RESULT 37
US-08-560-098A-53
; Sequence 53, Application US/08560098A
; Patent No. 5976841
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100.0%;
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SOFTWARE: Datentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/871,355A FILING DATE: 09-JUN-1997 CLASSIFICATION #435 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/GB95/02875 FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMS 101 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Georgia
COUNTRY: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      RPMS 101
                            ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION UNDRER: 31,284
REPRENCE/DOCKET UNDRER: RPMS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFRENCE/CDCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                              LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 amino acids
                                                                                                                                                                                                                                                                                                 : protein
NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                      TOPOLOGY: lin.
MOLECULE TYPE:
HYPOTHETICAL: N
US-08-637-759B-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 DYDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-871-355A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DYDA 4
                                                                                                                                                                                                                            LENGTH:
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100.0%; Score 23; DB 1; Length 244;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
APPLICANT: Little, Sheila P.
APPLICANT: No. 5733768ris, Franklin H.
TITLE OF INVENTION: PROTEASE AND RELATED DNA COMPOUNDS
NUMBER OF SECUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible |
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361, 395
FILING DATE: 22-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X8350A
TELEFAR: 317-277-1090
TELEFAR: 317-277-1090
TELEFAR: 317-277-1090
TELEFAR: 317-277-1090
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03.MAY-1996
CLASSIFICATION 0475
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
                                                            ALUNESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
STATE: Indiana
COUNTRY: United States
Mprimer
Mprimer
Mprimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 39
US-08-637-759B-92
Sequence 92. Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
TATLE OF INVENTION:
TATLE OF INVENTION:
CORRESPONDENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-361-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 DYDA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DYDA 4
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Gaps ö Length 257; 0; Indels Query Match
100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0;

Sequence 92, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:

; HYPOTHETICAL: US-08-871-355A-92

```
GENERAL INFORMATION:
APPLICANT: BRILES, David E.
APPLICANT: BRILES, David E.
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION OF TITLE OF INVENTION: INMUNOCOCCAL SURFACE PROTEIN A (PSPA)
FILE REFERENCE: 454312-2018
CURRENT APPLICATION NUMBER: US/08/446, 201B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 23; DB 3; Length 288; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 3; Length 288;
                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                    OPERALLING DATE:
SOFTWARE: Patentin Release --
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,949
FILLING DATE: 30-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPAX: (212) 840-333
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids

"VDF. amino acids
                                       SEE: Curtis, Morris & Safford, P.C. : 530 Fifth Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 1995-05-19
EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-05-20
EARLIER PILING DATE: 1994-05-20
EARLIER PLING DATE: 1994-02-09
EARLIER FILING DATE: 1993-04-20
EARLIER PELING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 07/656,773
EARLIER FILING DATE: 1991-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 288
                                                                                                        New York
United States of America
                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08446201B Patent No. 6042838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-08-446-201-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                          STREET: 530
CITY: New YC
STATE: New YC
COUNTRY: UN:
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||
|14 DYDA 17
                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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US-08-446-201-4
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                                           Gaps
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100.0%; Score 23; DB 3; Length 257; 100.0%; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 257;
                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 4; L4
100.0%; Pred. No. 4.8e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                         Sequence 92, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE PATERS:
STREET: 2800 One Atlantic Center
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08312949
Patent No. 6027734
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Wu, Hong Yin
TITLE OF INVENTION: MUCOSAL ADMINISTRATION OF
TITLE OF INVENTION: PNEUMOCOCCAL ANTIGENS
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8734
TELEFAX: (404) 873-875
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sil
                 Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                          |||||
60 DYDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111
60 DYDA 63
                                                                                  1 DYDA 4
                                                                                                                                                                                    RESULT 41
US-09-201-945-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-312-949-4
  Query Match
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Gaps

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Ouery Match
Best Local Similarity الاست
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14 DYDA 17
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                                 Gaps
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                                                                                                                                RESULT 44
US-08-072-070-4
; Sequence 4, Application US/08072070
; Patent No. 5476929
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: Yother, Janet L
; APPLICANT: Mobaniel, Larry S
; TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
; INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd
; STREET: Sulte 1203, 2001 Jefferson Davis Highway
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2202-0286
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible |
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/072,070
FILING DATE: 19930603
CLASSIFICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
RICH APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) $1-0378
TELEFAX: (703) $21-0378
TELEFAX: LURPAR WASHINGTON
INFORMATION FOR SEQ ID NO: 4:
EDWATH. PROSECTION NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aguence ... 575340.

Patent No. 575340.

Patent No. 575340.

APPLICANT: Briles, David E ...

APPLICANT: Yother, Janet L ...

APPLICANT: McDaniel, Larry S ...

APPLICANT: McDaniel, Larry S ...

APPLICANT: PROTEIN ...
       Pred. No. 5.5e+02;
Mismatches 0;
100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 45
US-08-469-434-4
Sequence 4, Application US/08469434;
Parent No. 5753463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 289 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
FRAGMENT TYPE: N-terminal
US-08-072-070-4
   Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
                                                                                       14 DYDA 17
                                                       1 DYDA 4
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14 DYDA 17
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100.0%; Score 23; DB 1; Length 289; 100.0%; Pred. No. 5.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,434
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,065
FILING DATE: UNMER: US/08/072,065
FILING DATE: US/08/072,065
FILING DATE: US/08/072,065
FILING DATE: US/07/835,698
FILING DATE: US/07/835,698
FILING DATE: US/07/835,698
FILING DATE: US/07/856,773
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 amino acids
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                                                                                                                              CITY: Aritus
STATE: Virginia
COUNTRY: U.S.A.
?IP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Search completed: February 6, 2003, 11:24:03 Job time: 11.3333 secs

Gaps

ó

Indels

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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-7un-2001
CLASSIFICATION: <u >cu <u <u >cu <u >cu <u <u >cu <u >cu <u <u <u >cu <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u >cu <u <u <u <u >cu <u <u >cu <u <u <u >cu <u <u >cu <u <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u <u <u >cu <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US OF FILING DATE: 03-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4554, App
Sequence 104, App
Sequence 105, Appl
Sequence 15, Appl
Sequence 5597, Ap
Sequence 16, Appl
Sequence 252, Appl
Sequence 4707, Appl
Sequence 6546, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 211, App
Sequence 11, Appl
Sequence 4443, Ap
Sequence 2, Appli
Sequence 5328, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                (without alignments)
15.202 Million cell updates/sec
                                                                                                                                     February 6, 2003, 11:22:09; Search time 5.83333 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // regnz_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
// cgnz_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
// cgnz_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 US-09-879-957-102

0 US-09-864-761-45554

0 US-09-879-957-104

0 US-09-948-080-15

0 US-09-9864-761-41344

0 US-09-788-626-516

0 US-09-788-626-516

0 US-09-738-626-74707

US-09-738-626-4707

US-09-738-626-6546

US-09-764-653-627
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US-09-815-242-5328
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US-09-738-626-4443
                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-712-363-211
                                                                                                                                                                                                                                                                                                                                                                                                  129505 seqs, 22169297 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:
                                                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT943-1
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Match
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                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                  sednence:
                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                    ritle:
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USING SAME

NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 1101-174

08/630,915

Sequence 5306. Ap Sequence 12632, A Sequence 12814, A Sequence 12514, A Sequence 135, Appl Sequence 1624, Ap Sequence 6267, Ap Sequence 1154, Ap Sequence 1154, Ap Sequence 1388, Ap Sequence 3589, Ap Sequence 3589, Ap Sequence 3589, Ap Sequence 5096, Ap Sequence 13797, A Sequence 13367, Ap Sequence 1336 T: SPARKS, Andrew B.
HOFFMAN, No. US20020034755Alh
KAY, Brian K.
FOWLKS, Dana M.
MCCONNELL, Stephen J.
INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND US-09-815-242-5306 US-09-815-242-12632 US-09-815-242-13749 US-09-815-242-12514 US-10-98-15-242-12857 US-10-033-297-135 US-09-777-430A-28 US-09-738-626-5624 US-09-738-626-5627 US-09-815-242-10772 US-09-925-300-1154 US-09-925-301-1138 US-09-741-669-353 US-09-744-870-504 US-09-738-626-3589 US-09-815-242-13792 US-09-815-242-13792 US-09-815-242-5096 US-09-738-626-508 US-09-815-242-13727 US-09-815-242-13367 US-10-081-859-2 US-09-738-626-6527 Sequence 102, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B. 100. 100. 100. 100. 100. Q. RESULT 1 US-09-879-957-102

Gaps

; 0

Indels

pat943-1.rapb

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APPLICANT: SPARKS, Andrew B.

APPLICANT: SPARKS, AND SPARKS, AND SPARKS, AND SPARKS, AND SPARKS, Dana M.

FOWLKES, Dana M.

MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
                                                                           OTHER INFORMATION: MAP TO AL157392.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.88

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.08

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.08
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 10; Length 38; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WEDLUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-879-957-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104, Application US/09879957 Patent No. US20020034755A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         vuery match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: USA
                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          US-09-864-761-45554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||
19 DYDA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-879-957-104
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY WICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY WICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR REPLICANTION NUMBER: US 60/20/456
PRIOR PELICATION NUMBER: US 60/20/456
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-09-37
PRIOR PELICATION NUMBER: PCT/US01/0066
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 10; Length 38; 100.0%; Pred. No. 40; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 45554 LENGTH: 38
                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-879-957-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR AFFLICATION NUMBER: FLI/USUL/UNGOS)
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45554, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.vv
-hac 4; Conservative
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US-09-864-761-45554
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Length 39;

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RESULT 6
US-09-864-761-41344
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12 DYDA 15
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US-09879-95
US-096879-957-96
Sequence 96, Application US/09879957
Sequence 96, Application US/09879957
Sequence 96, Application US/09879957
Sequence 96, Application US/09879957
Sequence 96, Application US/08020034755Alh
HOFPMAN, No. US/08020034755Alh
KAY, Brian K.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
MCCONNELL OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
USING SAME
USING SAME
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STARANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-879-957-96
              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 96:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-948-080-15
Sequence 15, Application US/09948080
Patent No. US20020102702A1
GENERAL INFORMATION:
100.08; Pr. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
--haq 4; Conserva
            Best Local Similarity
Matches 4; Conserv
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                                                                                         DYDA 8
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PAPILCANT: WAN DER OSTEN. CLAMS
APPLICANT: WAN DER OSTEN. CLAMS
APPLICANT: WAN DER OSTEN. CLAMS
APPLICANT: MANERY PETER KAN
PAPILCANT: MANITY: PETER KAN
TITLE OF INVENTIVE: PETER KAN
TO AN OFFICANT ON WORSE: US/9/9/40.08

SED TO NO. 10.
SED TO NO
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US-09-881-823-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 16
LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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0
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OTHER INFORMATION: EXPRESED IN LÜNG, SIGNAL = 2.1

OTHER INFORMATION: EXPRESED IN HEARY. SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BADLIT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2

OTHER INFORMATION: EST_HUMAN HIT: BF347885.1, EVALUE 7.00e-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 41344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 10;
illarity 100.0%; Pred. No. 71;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5597, Application US/09738626
Fublication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKGARA, SATOSHI
APPLICANT: NAKGARA, SATOSHI
APPLICANT: NAKGARA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: AVSHI, MISTRO
APPLICANT: TATELSHI, MACKO
APPLICANT: TATELSHI, MACKO
APPLICANT: TATELSHI, MACKO
APPLICANT: TATELSHI, NAKO
APPLICANT: TATELSHI, NAKO
APPLICANT: TATELSHI, NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SED ID NOS 5597
LIENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                 LENGTH: 69
                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                     FEATURE:
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Sequence 16, Application US/09881823

Patent No. US20020068066A1

GENERAL INFORMATION:
APPLICANT: ANDERSON, MAXWELL
APPLICANT: ANDERSON, MAXWELL
APPLICANT: WINA, RYAN
APPLICANT: WINA, LETITIA
APPLICANT: WINA, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION Wethod for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22651-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT PAPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 32
SUFTWARE PATENTIN VERSION 3.0
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; OTHER INFORMATION: Amino acid sequence of Protease m (Prom) catalytic
; OTHER INFORMATION: domain
US-09-796-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09796294

Patent No. US20020037581A1

GENERAL INFORMATION:
APPLICANT: O'Baiten, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D60200193

CURRENT APPLICATION NUMBER: US/09/796,294

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 09/618,259

NUMBER OF SEQ ID NOS: 72

SEQ ID NO !

LENGTH: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 10;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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8-09-833-790-252
; Sequence -252, Application US/09833790
; Patent No. US20020068288A1
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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ORGANISM: unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Murine
US-09-881-823-16
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Sequence 998, Application US/09925301

Patent No. US2002052308A1

GENERAL INFORMATION:

TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 1.7e+02;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SETKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKCI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKTHIRO
APPLICANT: SENOH, AKTHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE PETENTIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6546, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
COGANISM: Homo sapiens
US-09-925-301-998
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| 152 DYDA 155
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67 DYDA 70
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LENGTH: 184
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LENGTH: 165
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                APPLICANT: Lodes, Michael J.
APPLICANT: Mang, Tongtong
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REPERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT APPLICATION NUMBER: US/09/833,790
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 10;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4707, Application US/09738626
Publication No. US2020197605A1
GENERAL IMPORMATION:
APPLICANT: NAKGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: HAYASHI, NAKIO
APPLICANT: TYOKOI, HARUHIKO
APPLICANT: TYOKOI, HARUHIKO
APPLICANT: TYOKOI, HARUHIKO
APPLICANT: TYOKOI, HARUHIKO
APPLICANT: TKEDA, MASATO
APPLICANT: TKEDA, MASATO
APPLICANT: OCHAL, NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEO TD NACS 700cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4707
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 10v.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Homo sapiens
US-09-833-790-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-738-626-4707; Sequence 4707, A
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SEQ ID NO 4707
LENGTH: 165
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Gaps

RESULT 14 US-09-764-853-827

RESULT 12 US-09-925-301-998

Gaps

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1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (182); ; OTHER INFORMATION: Xaa equals any, of the naturally occurring L-amino acids US-09-764-853-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Sequence 827, Application US/09764853
Patent No. US200200652A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SEQ ID NO 827
LENGTH: 201
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100.0%; Score 23; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 221;
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100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: UCS/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-10-28
PRIOR FILING DATE: 2000-01-28
PRIOR PLING DATE: 2000-02-01
PRIOR PLING DATE: 2000-02-01
PRIOR PELICATION NUMBER: 60/110,844
PRIOR PELICATION NUMBER: 60/110,844
PRIOR PELING DATE: 1999-01-29
PRIOR PELING DATE: 1999-01-29
PRIOR PELING DATE: 1999-02-01
PRIOR PELING DATE: 1999-02-01
PRIOR PELING DATE: 1999-02-01
PRIOR PELING DATE: 1999-02-01
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
NUMBER OF SEQ ID NOS: 292
LENGTH:: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 211, Application US/09712363
Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-712-363-211
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Amino acid sequence of human protease m (hProM); OTHER INFORMATION: accession no. U62801
US-09-796-294-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                      APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D602COTP3
CURRENT APPLICATION NUMBER: US/09/796,294
CURRENT FILICATION NUMBER: US/09/796,294
PRIOR APPLICATION NUMBER: US 09/618,259
PRIOR PILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 11
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 10;
1larity 100.0%; Pred. No. 2.5e+02;
Conservative 0; Mismatches 0;
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100.0%; Score 23; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0;
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
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Publication No. US20020197605A1
GENERAL INFORMATION:
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                                                                                                                      Sequence 11, Application US/09796294
Patent No. US20020037581A1
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YOKOI, HARUHKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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191 DYDA 194
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97 DYDA 100
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                                                                           RESULT 16
US-09-796-294-11
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SEQ ID NO 4443
LENGTH: 252
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Gaps

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TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and North Title OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and ITTLE OF INVENTION: Using Them

FILE REFERENCE: 1043c2

CURRENT APPLICATION NUMBER: US/09/971,536

CURRENT FILING DATE: 2001-10-02

PRIOR FILING DATE: 2000-08-08

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 51

LENGTH: 301
  Length 267;
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramancto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: Z000-03-21
PRIOR FILING DATE: Z000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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                                                      Indels
Query Match 100.0%; Score 23; DB 10; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 4; Conservative 0; Mismatches 0;
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Amamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                Sequence 51, Application US/09971536
Patent No. US20020159976A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka
APPLICANT: Bloksberg, Leonard
APPLICANT: Lubbers, Mark
APPLICANT: Dekker, James
APPLICANT: Christensson, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Lactobacillus rhamnosus US-09-971-536-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holland, Ross
O'Toole, Paul
Reid, Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 21
US-09-815-242-5306
                                                                                                                                                 118 DYDA 121
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| 64 DYDA 67
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US-09-971-536-51
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APPLICANT:
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FARWICK, Mike, et al.
APPLICANT: FARWICK, Mike, et al.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE CYSQ GENE
FILE REPERENCE: 033201 WD 245
CURRENT APPLICATION NUMBER: US/09/987,446
CURRENT APPLICATION NUMBER: 2001-11-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 252;
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Carr, John D.
APPLICANT: Carr, John D.
APPLICANT: Carr, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yawamoto, Robert T.
APPLICANT: Yawamoto, Robert T.
APPLICANT: Yawamoto, Robert T.
APPLICANT: Wu, H. Howard
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA-011A
CURRENT APPLICATION NUMBER: 60/20/9415,242
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 23; DB 10; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 4; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5328, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-987-446-2
                                                                                                                                                                                                                   Sequence 2, Application US/09987446 Patent No. US20020115162A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus aureus
US-09-815-242-5328
                                                      178 DYDA 181
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                         1 DYDA 4
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US-09-987-446-2
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Gaps

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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Probaryotes
FILE REFERENCE: ELITRA.011A
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100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
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PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-02

PRIOR PLING DATE: 2000-12-02

PRIOR PRILING DATE: 2000-12-02

PRIOR PRILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: PASESEQ FOR WINGOWS VERSION 4.0

SED ID NO 13749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
COCATION: (1)...(318)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13749
                                                                                                                                                                                                    Sequence 13749, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12514, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 100.

Matches 4; Conservative
                                                                                                                                                                                US-09-815-242-13749
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161 DYDA 164
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168 DYDA 171
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APPLICANT:
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                                                                                                                                                 RESULT 23
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; Pred. No. 3.1e+02;
0; Mismatches 0; Indels (
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELTTRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
NUMBER: FASO ID NOS: 14110
SEOTWARE: FASES for Windows Version 4.0
SEOTWARE: PASES FOR WINDOWS PRIOR PRIOR
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100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASLESQ for Windows Version 4.0
SOFTWARE: 308
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5306
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Zyskind, Judith W.
Wall, Daniel
Trawlck, John D.
Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-815-242-12632
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Length 318; Indels

Gaps

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Brow, Mary Ann D.
TITLE OF INVENTION: Detection of Nucleic Acids By Multiple
Sequential Invasive Cleavages
Length 323;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ELAPPY disk
COMPUTER: ELAPPY disk
COMPUTER: ELAPPY DEC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-NO. US20020187486A1-2001
CLASSIFICATION NUMBER: US/09/350,597
FILING DATE: 09-Jul-1999
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/756,386
FILING DATE: 21-JON-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 21-JUL-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 21-JUL-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 21-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 21-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 21-JUL-1996
APPLICATION NUMBER: US OR DEC-1996
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                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
Score 23; DB 10;
Pred. No. 3.2e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: FORS-02736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-033-297-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.
Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 75, Application US/10033297
Publication No. US20020187486A1
GENERAL INFORMATION:
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      100.0%;
100.0%;
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                            167 DYDA 170
                                                                                                                                 1 DYDA 4
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APPLICANT: Askind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard Constructes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION UNMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR PILICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,338
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR PRIOR FILING DATE: 2001-02-16
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                          CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
COFTWARE: FRAESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12857, Application US/09815242 Patent No. US20020061569A1
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CRGANISM: Staphylococcus aureus
US-09-815-242-12514
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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US-09-815-242-12857
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167 DYDA 170
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LENGTH: 323
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Gaps

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173 DYDA 176
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                                                                   US-09-777-430A-28
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                                                                                                                                                                                                                                                                                           SEQ ID NO 28
LENGTH: 326
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                                                                                               Sequence 135, Application US/10033297
Publication No. US20020187486a1
GENERAL INFORMATION:
Lyamichev, Victor
Mast, Andrea L.
Brow, Mary Ann D.
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: No. US20020187486A1 Relevant TOPOLOGY: No. US20020187486A1 Relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-10-033-297-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: (NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 326 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                               SEQUENCES:
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Best Local Similarity
'-hac 4; Conserve
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173 DYDA 176
                                                                      RESULT 27
US-10-033-297-135
    1 DYDA 4
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1 DYDA 4

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APPLICANT: SKIZYPOZYNSKI, Zbigniew
APPLICANT: Allawi, Hatim T.
APPLICANT: Allawi, Hatim T.
APPLICANT: Allawi, Hatim T.
APPLICANT: Takova, Tsetska
APPLICANT: Takova, Tsetska
APPLICANT: Neir, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REPERENCE: FORS-04912
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn version 3.1
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100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
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FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PAPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PAPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIN Ver. 3.0
SEQ ID NO. 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5624, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
Sequence 28, Application US/09777430A Patent No. US2020128465Al GBNERAL INFORMATION: APPLICANT: Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5624
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Gaps

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LOCATION: (96)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (140)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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- LOCATION: (314)

- OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1154
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APPLICANT: CTEAG ROSEN,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: DC7/US00/05988
PRIOR APPLICATION NUMBER: E0/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1154

LENTH: 344
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                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 23; DB 10; Length 341;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10772
LENGTH: 3.41
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; Patent No. US20020151681A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecalis
US-09-815-242-10772
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Best Local Similarity ?
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NAME/KEY: SITE
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234 DYDA 237
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| 228 DYDA 231
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US-09-741-669-353
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: BLITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
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Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10772, Application US/09815242; Sequence 10772, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION: APPLICANT: Haselbeck, Robert, APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Trawlck, John D. APPLICANT: Trawlck, John D. APPLICANT: Trawlck, John D. APPLICANT: Trawnorto, Robert T.
                                                                                                                                                         Sequence 6267, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION: APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6267
                                                                                                                                                                                                                                                                            ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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215 DYDA 218
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    1 DYDA 4
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LENGTH: 339
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42 DYDA 45
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                                                                                                                                                    TYPE: PRT
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERBENCE: PALO6
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1694
SOFTWARE: PACHAIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 394;
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Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                   APPLICANT: POLISH, R. Allyn
APPLICANT: Ohlsen, Rari L.
APPLICANT: Ohlsen, Rari L.
APPLICANT: Ohlsen, Rari L.
APPLICANT: Orlsen, Rari L.
APPLICANT: Ohlsen, Rari L.
ATILE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REPERROCE: ELITRA, 0009A
CURRENT APPLICATION NUMBER: 02/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%; Score 23; DB 10;
Similarity 100.0%; Pred. No. 3.9e+02;
4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-925-301-1388; Sequence 1388, Application US/09925301; Patent No. US20020052308A1; GENERAL INFORMATION:
Sequence 353, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn :
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli
US-09-741-669-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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| 107 DYDA 110
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SEQ ID NO 353
LENGTH: 365
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                 LOCATION: (33)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (369); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-870-504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 504
LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 23; DB 10; Length 3 Similarity 100.0%; Pred. No. 4e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TATEISHI, NACKO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFREENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PRILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3589, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYASHI, MIKIRO
OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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283 DYDA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DAISON, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Ku, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-01-22
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-10-22
PRIOR FILING DATE: 2000-10-22
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illarity 100.0%; Pred. No. 4.2e+02;
Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60,253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60,257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PLICATION NUMBER: 60,269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5096
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; Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Salmonella typhi
US-09-815-242-13792
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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415 DYDA 418
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US-09-815-242-5096
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|12 DYDA 15
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                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: IDENATYOLS

TITLE OF INVENTION: PROKATYOLS

TITLE OF INVENTION: PROKATYOLS

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

FRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,625

PRIOR FILING DATE: 2000-05-36

PRIOR FILING DATE: 2000-10-33

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2001-10-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

FROM TOWN 10-24
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, Grant J.
APPLICANT: Trawick, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 0.11A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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  Sequence 10254, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13792, Application US/09815242 Patent No. US20020061569Al GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                           APPLICANT: Ohlsen, Mari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Escherichia coli
US-09-815-242-10254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 38
US-09-815-242-13792
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Gaps

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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Brevibacterium flavum
US-10-081-859-2
                                                                                                      NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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US-09-738-626-6527
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                                                                                                                                                                     LENGTH: 438
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                                                                                           APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARR: ASCII Text

APPLICATION NUMBER: US/09/765,272

FILING DATE: 2Jan_2001

CLASSIFICATION NUMBER: 08/961,083

FILING DATE: 2Jan_2001

CLASSIFICATION NUMBER: 08/961,083

FILING DATE: CANKNOWN>

APPLICATION NUMBER: 36/333

REFERENCE/GOCKET NUMBER: 36/333

REFERENCE/DOCKET NUMBER: 36/333

REFERENCE/DOCKET NUMBER: 36/333

REFERENCE/DOCKET NUMBER: 36/333

TELEPRONE: (301) 309-8504

TELEPRONE: (301) 309-8512

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 437;
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100.0%; Pred. No. 4.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID'NO: 70:
US-09-765-272-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6703, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NARAGAWA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
                                  Sequence 70, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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                                                                                                                                                                                                                            CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                     COUNTRY: USA
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Best Local Similarity
Matches 4; Conserv
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288 DYDA 291
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US-09-738-626-6703
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Patent No. US2002012012a1;
GENERAL INFORMATION:
APPLICANT: SUGINOTO, MASAKAZU
APPLICANT: SUGINOTO, MASAKAZU
APPLICANT: TTO, HISAO
TITLE OF INVENTION: PHOSPHOSERINE PHOSPHATASE GENE OF CORYNEFORM BACTERIA
FILE REFERENCE: 202044USO
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                        Length 438;
                                                                                                                                                         Indels
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                                                                                                100.0%; Score 23; DB 9; Le
lilarity 100.0%; Pred. No. 4.4e+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MAZOGNUH, MINOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ATASAHI, MINIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKI
APPLICANT: OZAKI, AKI
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/081,859
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 09/761,716
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: JP2000-023341
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6527, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICAMT: NAKAGAWA, SATOSHI
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313 DYDA 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 9; Length 455; ilarity 100.0%; Pred. No. 4.5e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-03-815-742-13/2/
Sequence 13727, Application US/09815242
Fatent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Oblisen, Rari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tawick, John D.
APPLICANT: Sunamoto, Robert T.
FILE REFERENCE: EllTRA.011A
CURRENT APPLICATION NUMBER: 60/207, 727
FRIOR APPLICATION NUMBER: 60/253, 625
FRIOR APPLICATION NUMBER: 60/253, 625
FRIOR APPLICATION NUMBER: 60/257, 931
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/257, 931
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/269, 308
FRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEO TD NO: 14727
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PELLOR DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATCHING DATE: 2000-08-03
SOFTWARE: PATCHING VET. 3.0
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; LOCATION: (1)...(472)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13727
                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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SEQ ID NO 13727
LENGTH: 472
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Oy 1 DYDA 4

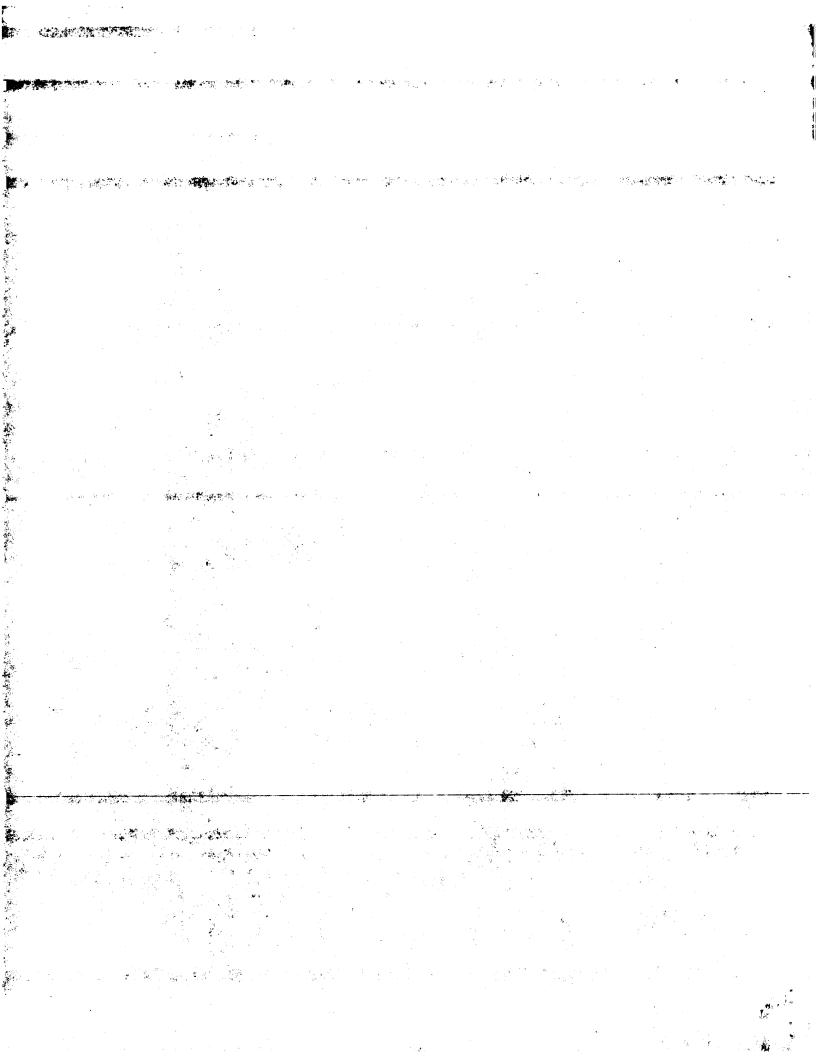
DESCRIPT 45

RESULT 45

SEQUENCE 13367

SEQUENCE 13687

SEQUENCE
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pat943-1.rapm

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Sequence 60, Appl
Sequence 60, Appl
Sequence 3652, Ap
Sequence 4801, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number of results predicted by chance to have a am or equal to the score of the result being printed, y analysis of the total score distribution.
                                                                                                                                                                      (without alignments)
19.366 Million cell updates/sec
                                                                                                                                            2003, 11:16:59 ; Search time 133.167 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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2: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*
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23: /cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-057-416-60
US-09-716-9648-60
US-60-160-209-3652
US-60-169-868-4801
PCT-USO0-09866A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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14
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127
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                                                                                                                                               February 6,
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13
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Match
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100.0
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APPLICANT: Yurieva, Olga
APPLICANT: Kuriyan, John
APPLICANT: C'Donnell, Michael E.
APPLICANT: O'Donnell, Michael E.
APPLICANT: Jeruzalmi, David
TITLE OF INVENTION: ENZYME DERIVED FROM THERMOPHILIC ORGANISMS THAT FUNCTION
NUMBER OF SEQUENCES: 116
               Sequence 36, Appl.
Sequence 36, Appl.
Sequence 2539, Appl.
Sequence 4129, Appl.
Sequence 4129, Appl.
Sequence 3514, Appl.
Sequence 102, Appl.
Sequence 102, Appl.
Sequence 3514, Appl.
Sequence 3510, Appl.
Sequence 3681, Appl.
Sequence 36701, Appl.
Sequence 36701, Appl.
Sequence 3681, Appl.
Sequence 3681, Appl.
Sequence 37, Appl.
Sequence 69, Appl.
Sequence 6915, Appl.
Sequence 6915, Appl.
Sequence 33, Appl.
Sequence 34, Appl.
Sequence 37, Appl.
Sequence 37, Appl.
Sequence 6815, Appl.
Sequence 37, Appl.
Sequence 574, Appl.
Sequence 37, Appl.
Sequence 584, Appl.
Sequence 37, Appl.
Sequence 37, Appl.
Sequence 584, Appl.
                                                                                                                                                                                                                                                                                                        Sequence 12882, A
Sequence 28441, A
Sequence 1476, Ap
Sequence 57408, A
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                                         PCT-US01-03800A-1476
US-09-270-767-57408
                                                                                                                                                                                                                                                                                                          US-60-360-039-12882
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60, Application US/09057228 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackensack
: New Jersey
RY: USA
                                                                                                                                                       1000.
                                                                          07601
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/143,202

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STATE STATE IN COMMENTATION:

STATE STATE IN COMMENTATION:

APPLICANT: Yuzhakov, Alexander

APPLICANT: Bruck, Irina

APPLICANT: Bruck, Irina

APPLICANT: Kuriyan, John

TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT

TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION NUMBER: US/09/716,964A

CURRENT APPLICATION NUMBER: US/09/716,964A

CURRENT APPLICATION NUMBER: 00/143,202

PRIOR APPLICATION NUMBER: 00/43,202

PRIOR APPLICATION NUMBER: 09/823,407

PRIOR APPLICATION NUMBER: 09/057,416

PRIOR APPLICATION NUMBER: 09/057,416

PRIOR APPLICATION NUMBER: 09/057,416

NUMBER OF SEQ ID NOS: 212

SEQ ID NO 60

LENGTH: 13
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GENERAL INFORMATION:
APPLICAMT: BOANZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOM 13
CURRENT APPLICATION NUMBER: US/60/160,209
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 4646
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3652
LENGTH: 20
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                Length 13;
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                                                                                                                                                                                                                                   100.0%; Score 23; DB 14; 100.0%; Pred. No. 2.8e+02;
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US-09-716-964A-60
; Sequence 60, Application US/09716964A
; GENERAL INFORMATION:
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                       90:
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                                                                                                                                                                                                           Query Match
Best Local Similarity luv...
                                                                     13 amino acids
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                     single
                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-057-416-60
                                                                                          TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-60-160-209-3652
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5 DYDA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yurieva, Olga
APPLICANT: Yurieva, Olga
APPLICANT: Kuriyan, John
APPLICANT: Kuriyan, John
APPLICANT: Commell, Michael B.
APPLICANT: Jeruzalmi, Davidel B.
TTILE OF INVENTION: FHAT FUNCTIONS AS A CHROMOSOMAL REPLICASE, PREPARATION AND USE
TITLE OF INVENTION: THAT FUNCTIONS AS A CHROMOSOMAL REPLICASE, PREPARATION AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,416
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-179 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 600-11-179 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/143,202
FILING DATE: 08-APR-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/823,407
FILING DATE: 08-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/823;407
ETLING DATE: 08-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60, Application US/09057416 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
STATE: New Jersey
COUNTR: 050
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
08-APR-1997
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-057-228-60
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                                                                                                                                                                                                                                                                                                                                                 LENGTH: 13 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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CITY: Ha
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Gaps

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Sequence 2726, Application US/60160209
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/160,209
CURRENT APPLICATION NUMBER: US/60/160,209
NUMBER OF SEQ ID NOS: 4646
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 2726
                                     TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTIENS AND USES TITLE OF INVENTION: THEREOF FILLE REFERENCE: CLOOULIS CURRENT APPLICATION NUMBER: US/60/160,209 CURRENT APPLICATION NUMBER: US/60/160,209 NUMBER OF SEQ ID NOS: 4646 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2607
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                                                                                                                                                                                                                                                                                                                           Length 24;
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US-08-263-921B-36
US-08-263-921B-36
Sequence 36, Application US/08263921B
GENERAL INFORMATION:
APPLICANT: CHANG, MING-TANG
TITLE OF INVENTION: OVEL PLANTS AND PROCESSES FOR
TITLE OF INVENTION: OPTAINING THEM
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: D S REWOLDT
STREET: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 27;
llarity 100.0%; Pred. No. 5.7e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 27; 100.0%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
      GENERAL INFORMATION:
                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-209-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: HUMAN
US-60-160-209-2726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UN
ZIP: 50244
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8 DYDA 11
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8 DYDA 11
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                                                                                                                                                                                                                                                                                             Sequence 4801, Application US/60169868
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TALE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOOL61
CURRENT APPLICATION NUMBER: US/60/169,868
CURRENT FILIA DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 6938
SOFTWARE: FASTSEQ for Windows Version 4.0
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GENERAL INFORMATION:
FAPFLICANT: SMITHKLINE BEECHAM CORPORATION
TITLE OF INVENTION:
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
CURRENT APPLICATION NUMBER: PCT/USO0/09866A
CURRENT APPLICATION NUMBER: US 60/129,073
PRIOR APPLICATION NUMBER: US 60/129,073
SOFTWARE: FASTEO for Windows Version 3.0
                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%; Score 23; DB 1; Length 21; Similarity 100.0%; Pred. No. 4.9e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 27;
100.0%; Pred. No. 4.6e+02;
ive 0; Mismatches 0;
                                                                             Query Match
100.0%; Score 23; DB 27;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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PCT-US00-09866A-10
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Best Local Similarity
Matches 4; Conservat
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-209-3652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
US-60-169-868-4801
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PCT-US00-09866A-10
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US-60-160-209-2607
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2 DYDA 5
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2 DYDA 5
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LENGTH: 20
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LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Gaps

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TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
            peptide
                                              ; ORGANISM: PAGE 11 T4
US-08-346-602A-36
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COUNTRY: US
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Best Local Similarity
        MOLECULE TYPE:
ORIGINAL SOURCE
                                                                                                                                                                                                           11 DYDA 20
                                                                                                                                                                                                                                                                                RESULT 11
US-09-118-990A-36
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GENERAL INFORMATION:
APPLICANT: KEELING, PETER L
APPLICANT: CHANG, MING-TANG
TITLE OF INVENTION: THEM
NUMBER OF SEQUENCES:
CORRESPONDENCE A3
CORRESPONDENCE A03
STREET: 2369 330TH ST BOX 500
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 6; Length 28; 100.0%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 50244
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PAtentIn Release #1:0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346 602A
FILING DATE: 29-NOV-1994
FLING APPLICATION DATA:
APPLICATION NUMBER: US 08/263/921
FLING APPLICATION NUMBER: US 08/263/921
FILING DATE: 21-JUN-1994
ATTOREX/AGENT INFORMATION:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/263,921B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                              ATTORNEY AFTELLATION DATE:

APPLICATION NUMBER: US/08/263,921B
FILING DATE: 21-JUN-1994
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: REWOLDT, DANA S
REGISTRATION NUMBER: 1.02.15
REFERENCE/DOCKET NUMBER: 1.02.15
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: (515)685-3574
TELEPHONE: (515)685-3574
TELEFAN: (515)685-2548
INFORMATION FOR SEQ ID NO: 36: SEGUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s
33,762
- 1.02,15A
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TELEPHONE: (515) 685-3574
TELEFAX: (515) 685-2548
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: REWOLDT, DANA S
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: PAGE 11 T4 US-08-263-921B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                  linear
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Gaps Gaps Sequence 36, Application US/09118990A
GENERAL INFORMATION:
APPLICANT: KEELING, PETER L
CHANG, MING-TANG
TITLE OF INVENTION: NOVEL PLANTS AND PROCESSES FOR OBTAINING ö .; 0 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/118,990A
FILING DATA:
APPLICATION CURNOWN>
PRIOR APPLICATION CURNOWN>
PRIOR APPLICATION NUMBER: US 08/346,602
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: US 08/263,921
FILING DATE: 21-JUN-1994 Length 28; Length 28; 0; Indels Indels 100.0%; Score 23; DB 7; 1 100.0%; Pred. No. 6.8e+02; 100.0%; Score 23; DB 15; llarity 100.0%; Pred. No. 6.8e+02; Conservative 0; Mismatches 0; 0; Mismatches CORRESPONDENCE ADDRESS:
ADDRESSEE: DANA REWOLDT ICI SEEDS
STREET: 2369 330TH ST BOX 500 REFERENCE/DOCKET NUMBER: 1.02.15A TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 685-3574 ORGANISM: PAGE 11 T4 SEQUENCE DESCRIPTION: SEQ ID NO: 36: US-09-118-990A-36 ATTORNEY/AGENT INFORMATION:
NAME: REWOLDT, DANA S
REGISTRATION NUMBER: 33,762 685-2548 LENGTH: 28 amino acids TYPE: amino acid STRANDEDNESS: single TELEFAX: (515) 685-2 INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS ZIP: 50244 COMPUTER READABLE FORM: MEDIUM TYPE: Flopp

RESULT 12

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PETCUSUL OUGS-13-07/01

Sequence 36/01, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Harzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: HUMAN PROPULCATION NUMBER: US 60/180,312
CURRENT FILING DATE: 2001-01-30
PRIOR PLING DATE: 26 may 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 60/236,366
PRIOR FILING DATE: 21 September 2000 (31.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/236,369
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/236,408
PRIOR FILING DATE: 21 September 2000 (30.06.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38837
SOFTWARE MOLECULAT Dynamics Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/08417872A
GENERAL INFORMATION:
APPLICANT: SPARKS, ANDREW B
APPLICANT: SPARKS, ANDREW B
APPLICANT: HOFFMAN, NOAH
APPLICANT: KAY, BRIAN K,
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOWAIN
TITLE OF INVENTION: OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                             Gaps
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96
OTHER INFORMATION: EST_HUMAN HIT: BF574717.1, EVALUE 1.00e-14
OTHER INFORMATION: SST_ROTHER INFORMATION: SWISSPROT HIT: P08442, EVALUE 7.40e-01
            Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 38;
                                                           Indels
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100.0%; Pred. No. 9.6e+02;
... wismarches 0;
       Query Match 100.0%; Score 23; DB 27;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 4; Conserv
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17 DYDA 20
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19 DYDA 22
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US-08-417-872A-55
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LENGTH: 38
                                                                                                           1 DYDA 4
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GENERAL INFORMATION:
TITLE BORDAZI, Vivion
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILLE REFERENCE: CLOO0127
CURRENT APPLICATION NUMBER: US/60/162,247
CURRENT FILLING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 5442
SEQ ID NO 4129
LENGTH: 31
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GENERAL INFORMATION:
GENERAL INFORMATION:
TOTAL SEQUENCE SEASON SERVICE SEASON SERVICES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/169,868
CURRENT APPLICATION NUMBER: US/60/169,868
CURRENT FILING DATE: 1999-12-09
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3774
LENGTH: 28
Sequence 2539, Application US/60160209
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIAND
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO0113
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 4646
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  h 100.0%; Score 23; DB 27;
Similarity 100.0%; Pred. No. 6.8e+02;
4; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: HUMAN
US-60-160-209-2539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Human
US-60-169-868-3774
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; ORGANISM: Human
US-60-162-247-4129
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US-60-162-247-4129
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2 DYDA 5
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2 DYDA 5
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LENGTH: 28
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KAY, Brian K.
FAMIKES, Dana M.
FOWLKES, Dana M.
MCONNELL, Stephen J.
MCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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EXPRESSED IN BONE MARROW, SIGNAL = 1

EXPRESSED IN PLACENTA, SIGNAL = 0.96

EXPRESSED IN ADULT LIVER, SIGNAL = 0.74

EXPRESSED IN FETAL LIVER, SIGNAL = 0.74

EXPRESSED IN BRAIN, SIGNAL = 0.74

EXPRESSED IN BRAIN, SIGNAL = 0.74

EXTENDAN HIT: BF54717.1, EVALUE 1.00e-14

SWISSPROT HIT: POB442, EVALUE 7.40e-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00668

PRIOR FILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 22; 100.0%; Pred. No. 9.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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RAPPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <UNFOWN>
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GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
HOFFMAN, Noah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MOTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
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COTHER INFORMATION:
US-09-864-761-45554
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US-09-879-957-102
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Sequence 42524, Application Us/Usou4/01

APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rack, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2000-02-04

PRIOR RILING DATE: 2000-02-04

PRIOR PELING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-07

PRIOR PULING DATE: 2000-09-07

PRIOR PULING DATE: 2000-09-07

PRIOR PULING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PULING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,872A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 8; 1
100.0%; Pred. No. 9.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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STRANDEDNESS: sin
                                               New York
U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: pro; HYPOTHETICAL: NO; ANTI-SENSE: NO US-08-417-8728-55
                                                                                                                                                                                                                                                                                                                   FILING DATE: 07 CLASSIFICATION:
                      New York
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                                                                                                  10036
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5 DYDA 8
                                                                         COUNTRY:
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
FILE REFERENCE: PB 0004 W0 6
CURRENT APPLICATION NUMBER: US/10/203,134
CURRENT FILING DATE: 2002-08-02
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER
                                                            Gaps
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100.0%; Score 23; DB 25; Length 38; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels
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US-10-203-134-36629
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PRIOR APPLICATION NUMBER: 05 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR FILING DATE: 05 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR PELING DATE: 03 August 2000 (30.08.00)

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 Cotober 2000 (27.09.00)

PRIOR PILING DATE: 37 September 2000 (27.09.00)

PRIOR PILING DATE: 21 September 2000 (27.09.00)

PRIOR PILING DATE: 21 September 2000 (27.09.00)

PRIOR PILING DATE: 31 September 2000 (30.06.00)

PRIOR PILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SED ID NOS: 38628

SOFTWARE: Molecular Dynamics Sequence Listing Engine

1 FRATILL 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%; Score 23; DB 26; Similarity 100.0%; Pred. No. 9.6e+02; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           Sequence 36629, Application US/10203134 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                         Conservative
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Best Local Similarity
                               Best Local Similarity
                                                                                                                                                                                                                                                       RESULT 20
US-10-203-134-36629
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US-10-203-136-36681
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19 DYDA 22
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19 DYDA 22
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     Query Match
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                                                         Matches
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN
FILE REFERENCE: PB 0004 WO 2
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; OTHER INFORMATION: SWISSPROT HIT: P08442, EVALUE 7.40e-01
US-10-182-993-35614
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US/10/182,993
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 20 3 August 2000 (30.08.00)
PRIOR APPLICATION NUMBER: US 60/203,366
PRIOR APPLICATION NUMBER: US 60/235,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,369
PRIOR APPLICATION NUMBER: US 60/236,4687
PRIOR APPLICATION NUMBER: US 60/236,4687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 30 June 2000 (30.06.00)
PRIOR FILING DATE: 37811
SOFTWARRE MOLECULAT DYNAMICS SEQUENCE LISTING ENGINE
LENGTH: 38
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100.0%; Pred. No. 9.6e+02;
tive 0; Mismatches 0;
                 FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MISIOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-8864/9741
TELERAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL
  APPLICATION NUMBER: US 08/630,915
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-879-957-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35614, Application US/10182993 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  LENGTH: 38 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 4; Conservative
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINCLE EXON NUCLEIC ACID PROBES USFUL
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINCLE EXON NUCLEIC ACID PROBES
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINCLE EXON NUCLEIC ACID PROBES
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINCLE EXON NUCLEIC ACID PROBES
ITILE DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/200, 456
PRIOR APPLICATION NUMBER: US 60/200, 600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 23; DB 26; Length 3 Best Local Similarity 100.0%; Pred. No. 9.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: SWISSPROT HIT: P08442, EVALUE 7.40e-01 US-10-203-137-36701
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; OTHER INFORMATION: SWISSPROT HIT: P08442, EVALUE 7.40e-01
US-10-203-139-35253
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                                                                                                                                                           OTHER INFORMATION: MAP TO AL157392.2 FEATURE:
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FEATURE:
OCHER INFORMATION: MAP TO AL157392.2
FEATURE:
                                                       TYPE: PRT
ORGANISM: Homo sapiens
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19 DYDA 22
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                                                                                                                                 FEATURE:
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GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Peno, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REPERENCE: PB 0004 WO.
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100.0%; Score 23; DB 26; Length 38;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: SWISSPROT HIT: P08442, EVALUE 7.40e-01 US-10-203-136-36681
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FRIOR APPLICATION NUMBER: US/10/203,137

PRIOR APPLICATION NUMBER: US/0/180/1312

PRIOR PILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207;456

PRIOR APPLICATION NUMBER: US 60/207;456

PRIOR APPLICATION NUMBER: US 09/832,366

PRIOR FILING DATE: 3 May 2000 (26.05.00)

PRIOR PILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PRILING DATE: 21 September 2000 (27.09.00)

PRIOR FILING DATE: 30 June 2000 (30:06.00)

NUMBER OF SEQ ID NOS: 38837

SEQ ID NO 36701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 36681
LENGTH: 38
                                                                                            PRIOR PELLING DATE: 2002-50-32.
PRIOR PELLING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207.456
PRIOR APPLICATION NUMBER: US 60/207.456
PRIOR PLING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 03 Aquast 2000 (03.08.00)
PRIOR FILING DATE: 03 Aquast 2000 (03.08.00)
PRIOR FILING DATE: 03 Aquast 2000 (03.08.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR PLILING DATE: 27 September 2000 (27.09.00)
PRIOR PLILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 31 September 2000 (21.09.00)
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38578
FILE REFERENCE: PB 0004 WO 3
CURRENT APPLICATION NUMBER: US/10/203,136
CURRENT FILING DATE: 2002-08-02
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ORGANISM: Homo sapiens
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US-10-203-137-36701
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19 DYDA 22
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HOFFMAN, Noah
KAY, Brian K.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
MCCONNELL DOLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPA: DC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFTCATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 39;
                                                                                                                                 Length 39;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                             100.0%; Score 23; DB 8; 100.0%; Pred. No. 9.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 22; 100.0%; Pred. No. 9.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. LESLIB.
REGISTRATION NUMBER: 18, 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDENESS: <UNKnown>
TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-879-957-104
                                                                                                                                                                                                                                                                                                                                                Sequence 104, Application US/09879957
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                       Conservative
TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserv
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                                                 HYPOTHETICAL:
ANTI-SENSE: N
US-08-417-872A-57
                                                                                                                                                                                                                                                                                                             RESULT 26
US-09-879-957-104
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5 DYDA 8
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S DYDA
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                                                                                                                         APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: And Uses Thereof
FILE OF INVENTION: and Uses Thereof
FILE REPRENCE: CLOO0122
CURRENT APPLICATION NUMBER: US/60/161,932
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 2626
SOFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SPARKS, ANDREW B
APPLICANT: HOFFMAN, NOAH
APPLICANT: KAY, BRIAN K.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN
TITLE OF INVENTION: OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/417,872A
FILING DATE: 07-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 27;
100.0%; Pred. No. 9.6e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(38)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-161-932-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                      Sequence 1951, Application US/60161932 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/08417872A GENERAL INFORMATION:
APPLICANT: SPARKS, ANDREW B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELEPHONE: 212-790-9090
TELERX: 66141 PENNIE
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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LENGTH: 39 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STRATE: New York
COUNTRY: U.S.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 DYDA 32
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28 DYDA 31
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                                                                                                            APPLICANT: SPARKS, ANDREW B
APPLICANT: HOFFMAN, NOAH
APPLICANT: KAY, BRIAN K.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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KAY, Brian K.
FOWLKES, Dana M.
MCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible |
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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LANDRESS:
|
| EBT: Pennie & Edmonds |
| EBT: 1155 Avenue of the Americas |
| Wew York |
| New York |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101-193
US-08-417-872A-49; Sequence 49, Application US/08417872A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872.
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-971/8864
INFORMATION FOR SEG ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96, Application US/09879957
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-417-872A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||
DYDA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 28
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Sequence 9365, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEP
TITLE OF INVENTION: DECORDED THEREBY
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 9365
LENTH: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 41;
                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: CURRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Location 1..41 / Ceres Seq. ID 1030234 US-09-513-996A-9365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 22;
100.0%; Pred. No. 1e+03;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 19;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915

FILING DATE: 0.3-APPL-1966

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELERX: (612) 790-9090

TELEX: 6644 PENNIE

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARATERISTICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: UNSURE
LOCATION: 1..41 /
OTHER_INFORMATION: any n or Xaa = unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-879-957-96
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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Best Local Similarity 100...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-513-996A-9365
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DYDA 8
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APPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
ATTLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd
STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                 ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,852
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/247,491
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 6; 100.0%; Pred. No. 1.2e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/835,698
FILING DATE: 12-FEB-1992
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/247,491
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
                                                                                                                                             COMPTER U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity الاست.
الا Conservative بالم
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COUNTRY: U.S.A.
ZIP: 2202-0266
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
      TITLE OF INVENTION: ST
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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US-08-247-491-3
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                                                                                                      Arlington
                                                                                                                              STATE: Virginia
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14 DYDA 17
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                            Sequence 68915, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REPERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 68915
LENGTH: 41
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Sequence 5748, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheelav
TITLE OF INVENTION: Thereby
FILE REPERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT APPLICATION NUMBER: S000-07-21
NUMBER OF SEQ ID NOS: 9131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Location 1..41 / Ceres Seq. ID 2185473 US-09-513-996A-68915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 19;
ilarity 100.0%; Pred. No. 1e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..41 /
OTHER INFORMATION: any n or Xaa = unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.41
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.41
OTHER INFORMATION: Ceres Seq. ID 1394958
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US-08-247-491-3
Sequence 3, Application US/08247491
GENERAL INFORMATION:
APPLICANT: Biles, David E
HAPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
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Matches 4; Conservative
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NAME/KEY: misc_feature
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Best Local Similarity
'-hes 4; Conserv?
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                          US-09-513-996A-68915
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US-09-620-394B-5748
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Gaps

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1 DYDA 4
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GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDaniel L
APPLICANT: McDaniel L
TILLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                 100.0%; Score 23; DB 8; Length 45; 100.0%; Pred. No. 1.2e+03;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,626
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
TELEOCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDRESSEE: Shoemaker and Mattare, Ltd
STREET: Sulte 1203, 2001 Jefferson Davis Highway
CITY: Arlington
STATE: Virginia
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ilarity 100.0%; Pred. No. 1.2e+03
Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                         Mismatches
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APPLICATION NUMBER: US 07/656,773 FILING DATE: 15-FEB-1991 | TELECOMMUNICATION INFORMATION: TELEDEHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                     .
                                                     TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 annho acids
TYPE: annho acids
TYPE: annho acids
TYPE: 11near
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TELEFAX: (703) 521-0378
TELEX: LUKPAY WASHINGTON
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
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ZIP: 22202-0286
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Best Local Similarity
Matches 4; Conserv
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Sequence 3984, Application US/09450969
(GENERAL INFORMATION:
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOC
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOC
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOC
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: PATH99-09A
CURRENT APPLICATION UNMER: US/09/450,969
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 7544
LENGTH: 46
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                                           APPLICANT: BORDAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
TITLE OF INVENTION: THERENE ENCODING HUMAN KINASE PROTIENS AND USES
FILE REFERENCE: CL000134
CURRENT PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 1302
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 951
LENGTH: 45
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US-10-008-524A-154
US-10-008-524A-154
Sequence 154, Application US/10008524A
Sequence 154, Application US/10008524A
Sequence 155, Application US/10008524A
TITLE OF INVENTION: URROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIRUSES
FILE REFERENCE: 18396/1074
CURRENT APPLICATION NUMBER: US/10/008,524A
CURRENT FILING DATE: 1999-05-18
PRIOR FILING DATE: 1999-05-18
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.2e+03;
Conservative 0; Mismatches
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Sequence 951, Application US/60163062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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SEQ ID NO 154
LENGTH: 47
TYPE: PRT
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US-09-450-969-3984
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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US-60-163-062-951
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; LOCATION: (1)...(51); CTHER INFORMATION: Xaa = Any Amino Acid US-60-177-571-4760
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Best Local Similarity
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ORGANISM: HUMAN
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                Length 47;
                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURREMY APPLICATION DATA: US/08/651,136A FILING DATE: 21-MAY-1996
100.0%; Score 23; DB 24; J
100.0%; Pred. No. 1.2e+03;
viematches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 10; 100.0%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                              APPLICANT: Schulein, Martin
APPLICANT: Andersen, Lene N.
APPLICANT: Lassen, Soren F.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Lange, Lene
APPLICANT: Intara, Ruby I.
APPLICANT: Intara, Michiko
APPLICANT: Takagi, Shinobu
TITLE OF INVENTION: Novel Endoglucanases
NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58, Application US/10007521
GENERAL INFORMATION:
APPLICANT: Schulein, Martin
Andersen, Lene N.
Lassen, Soren F.
Kauppinen, Markus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         Sequence 58, Application US/08651136A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Nielsen, Ruby I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 amino acids
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-651-136A-58
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                   Query Match
Best Local Similarity
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23 DYDA 26
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US-10-007-521-58
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                                                 Matches
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Sequence 4760, Application US/6017571

Sequence 4760, Application US/6017571

Sequence 4760, Application US/6017571

Sequence 4760, Application US/6017571

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIT ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/177,571
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 5082
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                        COUNTER TEADLE States of America
ZIP: 10174-6401
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPA:DIS-
COMPUTER: TBM PC COMPA:DIS-
COMPUTER: DEADLE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 49;
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                                                                                                     ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 24;
100.0%; Pred. No. 1.3e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TITLE OF INVENTION: Novel Endoglucanases NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136
FILING DATE: 21-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-10-007-521-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                          STATE: New York
                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserva
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Score 23; DB 27; Length 51; Pred. No. 1.3e+03;

100.0%; 100.0%;

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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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PCT-US01-03800A-1476
; Sequence 1476. Application PC/TUS0103800A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; TILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: PCT/US01/03800A
; CURRENT APPLICATION NUMBER: 09/560,875
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR PILING DATE: 2000-04-27
; PRIOR PILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1476
; LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 58;
                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO CHR3.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: SYPRESSED IN HELA, SIGNAL = 1.2
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                                    FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(58)
COTHER INFORMATION: Xaa = any amino acid or nothing
PCT-US01-03800A-1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 24; 100.0%; Pred. No. 1.4e+03;
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 57408, Application US/09270767; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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Best Local Similarity
Thes 4; Conserve
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Best Local Similarity
Matches 4; Conserv
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US-09-270-767-57408
                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATIONS OTHER INFORMATIONS-10-029-386-28441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYDA 23
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yainfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blate, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12882
LENGTH: 53
                                                                                                                                    RESULT 41

US-10-015-127-10406

Sequence 10406, Application US/10015127

GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Bower, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
FILE REFERENCE: 38-10/15806)B
CURRENT APPLICATION NUMBER: US/10/015,127

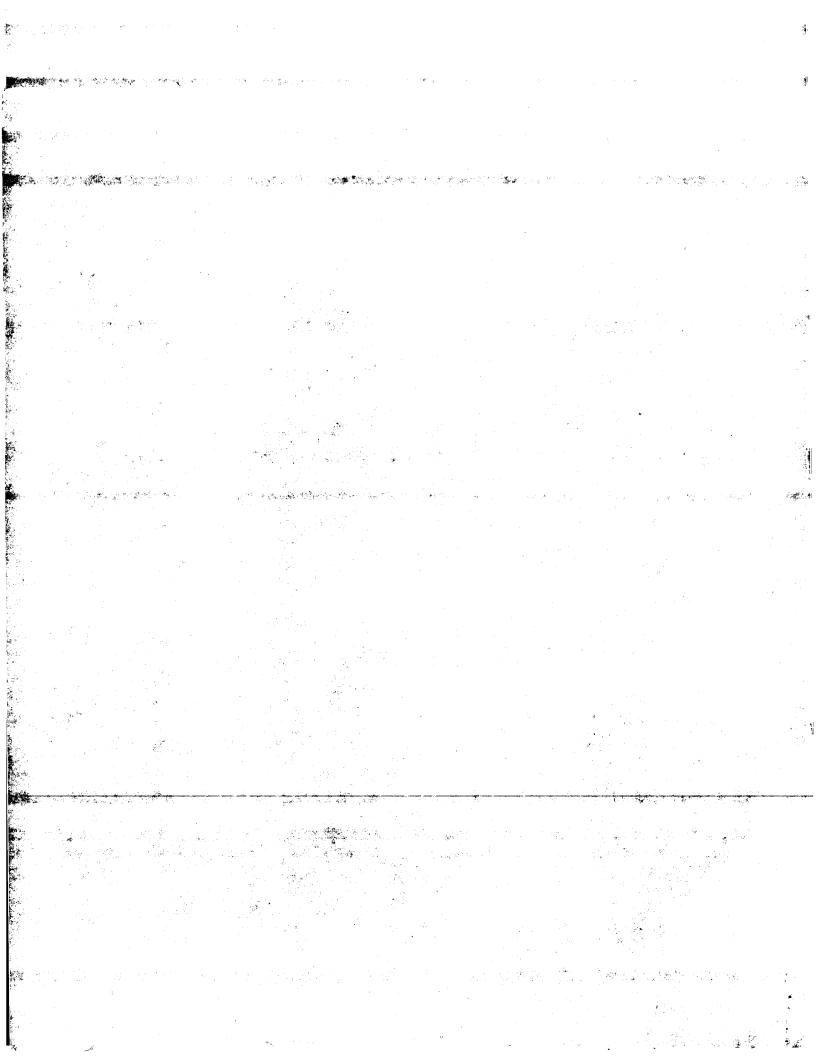
CURRENT FILING DATE: 2001-10-29
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357

SEQ ID NO 10406

LENGTH: 52
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100.0%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
    Mismatches
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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US-60-360-039-12882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Sphingomonas elodea US-10-015-127-10406
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    Conservative
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Matches 4; Conserv
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Best Local Similarity
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US-60-360-039-12882
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US-10-029-386-28441
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22 DYDA 25
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5 DYDA 8
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                                          DYDA 4
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFRENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: patentIn Ver. 2.0
; SOFTWARE: PATENTING BOTE: 1998-03-17
; TYPE: PRT
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57408
                                                                                                                                                                                                                                                                                                                          Gaps
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0
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                            1 DYDA 4
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7 DYDA 10
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 6, 2003, 11:16:04; Search time 10.5 Seconds (without alignments) 36.623 Million cell updates/sec Run on:

PAT943-1 23 1 dyda 4 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

757

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	probable transcrip	P5 protein - human	hypothetical prote	Q,	hypothetical prote		hypothetical 10.2K	hypothetical prote	Ig heavy chain V r	ribosomal protein	hypothetical prote				hypothetical prote	Ω	hypothetical prote	gene 17 protein -	aspartic proteinas	nitrogen fixation	hypothetical prote	hypothetical prote	ribosomal protein	transcription regu	hypothetical profe	÷	hypothetical prote	probable secreted	hypothetical prote
SUMMARIES	OI	\$77832	JW0095	D98266	AE3018	AD3215	H70721	JH0445	A96968	803306	E75531	D70970	F90686	B85537	AI0048	F70530	D87037	T27821	W1BP22	S24187	AF1985	G69903	AG3321	T01654	H87435	C84357	S19976	T12731	7.1	B70549
	Length DB				67 2															103 2						109 2		112 2		
dр	Query Match 1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	•	100.0
	Score	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
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conserved hypothet SH3 binding glutam	19 Neavy Chain v i hypothetical prote nitrogen regulator hypothetical prote	hypothetical prote conserved hypothet degenerate transpo	coat protein - pha conserved hypothet 13kda differentiat hypothetical prote	hypothetical prote ribosomal protein ribosomal protein
D87301 JE0178	D30340 AB1425 G96983 F87429	F84355 G87615 E97875	VCBPP1 AG2739 E97520 F70659	T04904 R5BY25 S30000
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30 31	3 8 3 8 3 4 3 8	36 37 38	39 40 42	43 44 55

ALIGNMENTS

RESULT 1 \$77832 probable transcription elongation factor - Mycoplasma capricolum (fragment) N,Alternate names: protein MC277 C;Species: Mycoplasma capricolum C;Date: 09-0ct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000	
C; Accession: S77832; S48616 R; Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbe Mol Mirchiol 16, 955-967, 1995	15e
the Mycoplasma capricolum genome: a minimal cell reveals its S77739; MUID:96059641; PMID:7476192	g s:
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-44 <bor></bor>	
A;Cross-references: EMBL:233203; NID:9541713; PIDN:CAA83788.1; PID:9950075 A;Experimental source: ATCC 27343 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994 C;Genetics:	994
A;Genetic code: SGC3 C;Superfamily: transcription elongation factor greb C;Keywords: transcription factor	
Query Match 100.0%; Score 23; DB 2; Length 44; Best Local Similarity 100.0%; Pred. No. 67; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	7.
Qy 1 DYDA 4 	
WO 10 67	
RESULT 2 JW0095 P5 protein – human (fragments)	
C;Species: Homo sapiens (man) C;Date: 03-U11-1998 #sequence_revision 10-Jul-1998 #text_change 10-Jul-1998	
C, ACCCS 1201. 1800. C. Aebersold, R.; Martin, B.M.; Merril, C.R.; Hood, L. R;Harrington, M.C. Electrophor. 3, 229-234, 1993 A;Title: Identification of a brain-specific human cerebrospinal fluid qlycoprotei	tei
A; Reference number: JW0095; MUID:94032630; PMID:7692978 A; Accession: JW0095 A; Status: preliminary A; Molecule type: protein A; Residues: 1-56 <har></har>	all the management of
Query Match 100.0%; Score 23; DB 2; Length 56; Best Local Similarity 100.0%; Pred. No. 87; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Gaps

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erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordor
                                                                                                                                                                                            Aritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A; Reference number: AB2577; PMID:11743193
A; Accession: AD3215
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-68 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. Species: Mycobacterium tuberculosis (strain H37RV)
C. Species: Mycobacterium tuberculosis
C. Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
R. Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gol; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Genlies, S.; Hamlin, N.; Holry Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Matthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A. Title: Deciphering the biology of Mycobacterium tuberculosis from the complete of My Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule type: DNA A;Residues: 1-85 <COL> A;Cross-references: GB:Z78020; GB:AL123456; NID:g3261625; PIDN:CAB01471.1; PID:e25:A;Experimental source: strain H37Rv A;Genetics: A;Gen
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Accession: JH0445
A; Croux, C; Garcia, J.L.
Gene 104, 25-31, 1991
A; Title: Sequence of the lyc gene encoding the autolytic lysozyme of Clostridium a A; Reference number: JH0441; MUID:92009192; PMID:1916274
A; Accession: JH0445
A; Accession: JH0445
A; Accession: JH0445
A; Accession: JH0441; MUID:92009192; PMID:1916274
A; Accession: JH0445
A; Accession: JH0445
A; Experimental source: ATCC 824
                                                                                                                                                                                                                                                                                                                                                                                                            A/Cross-references: GB:AE008687; PIDN:AAL46138.1; PID:g17743905; GSPDB:GN00188 A/Experimental source: strain C58 (Dupont) C;Genetics: A;Gene: Atu5451 A;Genome: plasmid
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Pred. No. 1.1e+02;
Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+02;
Live 0; Mismatches 0;
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Local Similarity 100.0%;
les 4; Conservative 0;
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Best Local Similarity

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33 DYDA 36
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Matches 4;
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                                                                                                                                                                                                                                  C. Species: Agrobacterium tumefaciens
C. Species: Agrobacterium tumefaciens
C. Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C. Accession: D99266
C. Accession: D99266
A. Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Reference number: A97359; PMID:11743194
A.; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A.; Status: preliminary
A.; Molecule type: DNA
A.; Residues: 1-67 < KUR>
                                                                                                                                                                                                                       - Agrobacterium tumefaciens (strain C58, Cere
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hypothetical protein Atu5451 [imported] - Agrobacterium tumefaciens (strain C58, Dupont hypothetical protein tumefaciens .
C.Species: Agrobaccerium tumefaciens .
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 (C; Accession: AD3215 ... Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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A;Cross-references: GB:AE008689; PIDN:AAL44563.1; PID:g17742179; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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D98266
hypothetical protein AGR_L_2160 [imported]
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Best Local Similarity 100.00
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Best Local Similarity
Matches 4; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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286, 1571-1577, 1999
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70 DYDA 73
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42 DYDA 45
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000
C;Accession: E75531
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                     CAccession: A96968
R;Nolling, J., Brateron, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tig heavy chain V region (6188) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: JL0046; S03306
R;Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independentl
A;Reference number: JL0043; MUID:88258372; PMID:2455014
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A:Molecule type: DNA
A:Residues: 1-86 <KUR>
A:Residues: 1-86 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78532.1; PID:g15023419; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                 hypothetical protein CAC0553 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                       Gaps
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tive 0; Mismatches 0;
100.0%; Score 23; DB 2; I
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ive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.5e+02;
Conservative 0; Mismatches 0;
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A; Residues: 1-90 <VAN>
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A;Molecule type: DNA
A;Residues: 1-91 - WHI>
A;Cross-references: GB:AE000513; NID:g6458011; PIDN:AAF09921.1; PID:
A;Experimental source: strain R1
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A;Gene: DR0341
A;Map position: 1
C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal prote
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A;Experimental source: strain H37Rv
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R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Har
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7] and A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv3357 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-7011-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: D70970
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
R; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID:98295987; PMID:9634230
A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
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A.Molecule type: DNA
A.Molecule type: DNA
A.Cross-references: GB:BA000007; PIDN:BAB33885.1; PID:g13359919; GSPDB:GN00154
A.Experimental source: strain O157:H7, substrain RIMD 0509952
C.Genetics:
A.Gene: ECS0462
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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Best Local Similarity
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                                                             A; Accession: E75531
A; Status: preliminary
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B85537
hypothetical protein ECS0462 [imported] - Escherichia coli (strain O157:H7, substrain ED C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
R; Perran, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Natitle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: B85537
A; Accession: B85537
A; Accession: B85537
A; Molecule type: DNA
A; Residues: 1-93 <CTO>
A; Cross-references: GB:AE005174; NID:g12513261; PIDN:AAG54758.1; GSPDB:GN00145; UWGP:205
C; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetic
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Cipecies: Yersinia pestis
Cipecies: Yersinia pestis
Cipate: 02-Nov-2001 #text_change 02-Nov-2001
CiAccession: A10048
Cipate: 02-Nov-2001 #text_change 02-Nov-2001
CiAccession: A10048
Cipate: 02-Nov-2001 #text_change 02-Nov-2001
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C;Species: Mycobacterium tuberculosis |
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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100.0%; Score 23; DB 2; Length 93
100.0%; Pred. No. 1.5e+02;
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100.0%; Pred. No. 1.5e+02;
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C;Accession: F70530
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Accession: F70530
A;Accession: F70530
A;Accession: F70530
A;Accession: E70530
A;Genetics: DNA
A;Molecule type: DNA
A;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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A;Residues: 1-100 <STO>
A;Cross-references: GB:AL450380; NID:g13093046; PIDN:CAC31407.1; GSPDB:GN00147
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C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C.Accession: 127821
R.McMurray, A.
Submitted to the EMBL Data Library, April 1996
A.Accession: 127821
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: Drall A.Status: DNA
A.Residues: 1-102 <a href="https://www.nca.mc/mc/mc/">wm.L.A.Coss: references: EMBL:270757; PIDN:CAA94799.1; GSPDB:GN00023; CESP:ZK287.3
A.Experimental source: clone 2K287
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100.0%; Pred. No. 1.7e+02;
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P. H

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aspartic proteinase inhibitor - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
C;Accession: 324187
R;Strukelj, B.; Pungercar, J.; Mesko, P.; Barlic-Maganja, D.; Gubensek, F.; Kregar, I.;
Biol. Chem. Hoppe-Seyler 373, 477-482, 1992
A;Title: Characterization of aspartic proteinase inhibitors from potato at the gene, cDR A;Reference number: S23961; MUID:92384955; PMID:1515078
A;Reference number: S23961; MUID:92384955; PMID:1515078
A;Reference number: S23961; Muid: A;Reference number: S23961; Muid: A;Reference number: S23961; Muid: C,Superfamily: campared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-103 <-STR>
C;Superfamily: cathepsin D inhibitor
C;Seywords: aspartic proteinase inhibitor
F;64-73/Disulfide bonds: #status predicted
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C;Dace: 31-Mar-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Dacession: 304246
Mol. Biol. 207, Walloy, D.C.; Poteete, A.R.
A:Title: Genetic structure of the bacteriophage P22 P(L) operon.
A:Reference number: S04245; MuID:8929845; PMID:2738922
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A;Residues: 1-103 <SEM>
A;Cross-references: EMBL:X15637; NID:g15646; PIDN:CAA33650.1; PID:g15650
A;Note: the authors translated the codon GGT for residue 26 as Gln
C;Genetics:
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nitrogen fixation protein [imported] – Nostoc sp. (strain PCC 7120)
A;Gene: CESP:ZK287.3
A;Map postLiton: 5
A;Introns: 57/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK287.3
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                                                                                                                            Length 102,
                                                                                                                         ; Score 23; DB 2; ]; Pred. No. 1.7e+02; 0; Mismatches 0;
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C,Superfamily: phage P22 gene 17 protein
                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
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Best Local Similarity
Matches 4; Conserv
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| 52 DYDA 55
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35 DYDA 38
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| 17 DYDA 20
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C; Species: Nostoc sp.
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AF1985
F; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; I
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Ta
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacter
A; Reference number: AB1807; WUID:21595285; PMID:11759840
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 28-Jul-2000
C;Accession: G69903
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.,
C; Brop, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.
A; Epflich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferra
Natyre 390, 249-256, 1997
Aruthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.;
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hull,
Necter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lar,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadale, Y.; Sato, T.; Sakuhors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uci
T.; Winters, P.; Wippet, A.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Attle: The complete genome sequence of the Gram-positive bacterium Bacillus sub.
A;Accession: G69903
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DMA.
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A;Cross-references: GB:299114; GB:AL009126; NID:92634230; PIDN:CAB13855.1; PID:e1<sup>1</sup>
A;Experimental source: strain 168
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A; Experimental source: strain PCC 7120
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C;Superfamily: Bacillus subtilis hypothetical protein yodL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: nifW
C,Superfamily: nitrogenase nifW chain
                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-105 < KUR>
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24 DYDA 27
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Best Local Similarity
Matches 4; Conserv
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A; Molecule type: DNA
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DYDA 33
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|DYDA 71
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                            Query Match
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R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Jaub, M.T.; DeBOy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon D, J.; Ermolaeva, M.; White, O.; Salzaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                    C;Accession: AG3321
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002.
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3321
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 ckUR>
A;Residues: 1-107 ckUR>
A;Residues: Sexperimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Zea mays (maize)
C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C; Accession: 701654
A; Reference number: Z14371
A; Accession: 701654
A; Accession: 701654
A; Accession: 10-Final A; Accession: 701654
A; References: EMBL: AFFINA
A; Residues: 1-109 *FINA
A; Residues: 1-109 *FINA
A; Residues: 1-109 *FINA
C; Superimental source: Strain 7X5585 |
C; Superimental source: Strain 7X5585 |
C; Superimental source: Inbosomal protein | L23a
C; Superfamily: rat ribosomal protein | L23a
C; Superfamily: rat ribosomal protein | L23a
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A; Molecule type: DNA
A; Residues: 1-109 <STO>
A; Cross-references: GB: AEO05673; NID; 913422882; PIDN: AAK23484.1; GSPDB: GN00148
C; Genetics:
A; Gene: CC1505
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
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100.0%; Pred. No. 1.8e+02;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosomal protein L23 - maize (fragment)
N;Alternate names: ribosomal protein L25
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100.0%;
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Best Local Similarity
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DYDA 99
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62 DYDA 65
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C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 0.2-Feb-2001 #sequence_revision 0.2-Feb-2001 #text_change 0.2-Feb-2001
C; Accession: C84357
R:NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; La; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G., Jung, K. H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T. A; Reference number: A84160; MUID: 20504483; PMID: 11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE004437; NID: 910581492; PIDN: AAG20223.1; GSPDB: GN00138
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C;Species: Methanobacterium phage psiM2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         If kappa chain V region (M-T413) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Peb-1995 #sequence_revision 06-Peb-1995 #text_change 21-Jan-2000
C;Accession: S19976
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EWBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19976
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A; Residues: 1-112 <WEL>
A; Cross-references: EMBL:X65093; NID:952298; PIDN:CAA46221.1; PID:952299
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 0;
Score 23; DB 2;
Pred. No. 1.8e+02;
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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Length 112;

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100.0%; Score 23; DB 2; I 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0;
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Ig heavy chain V region (174.3F4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
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C; Superfamily: hypothetical protein H10925
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                                                                                   Conservative
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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27 DYDA 30
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                                       Query Match
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C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Accession: B70549
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Authors: Special minary the biology of Mycobacterium tuberculosis from the complete genome A; Accession: B70549
A; Accession: B70549
A; Accession: B70549
A; Accession: B70549
A; Residues: 1-112 ccCu.>
A; Residues: 1-112 ccCu.>
A; Cross-references: GB:295558; GB:AL123456; NID:g3261781; PIDN:CAB08970.1; PID:e1299976; A; Genetics:
A; Genetics:
A; Genetics:
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R.Cole, S.T.; Edglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
RAthors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A.Hathors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A.Title: Massive gene decay in the leprosy bacillus.
A.Accession: R87193
A.Accession: F87193
A.Accession: F87193
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-112 <STO>
A.Residues: 1-112 <STO>
C.Genetics:
C.Genetics:
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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27 DYDA 30
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Matches
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RESULT 30
D87301
conserved hypothetical protein CC0421 [imported] - Caulobacter crescentus
conserved hypothetical protein CC0421 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: D87301
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelbe
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.,
D.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Fitle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87301
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-114 <STO>
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C; Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
C; Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
C; Accession: JEOJ78 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
R; Egeo, A.; Mazzocco, M.; Arrigo, P.; Vidal-Taboada, J.M.; Oliva, R.; Pirola, B.;
Biochem. Biophys. Res. Commun. 247, 302-306, 1998
A; Title: Identification and characterization of a new human gene encoding a small A; Reference number: JEOJ78; MUID:98308110; PMID:9642120
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C; Genetics:
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A;Residues: 1-114 <EGE>
A;Cross-references: GB:AF042081; NID:g3337419; PIDN:AAC27445.1; PID:g3337420
C;Genetics:
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C;Superfamily: human SH3 binding glutamate-rich protein
F;59-67/Region: proline-rich SH3 binding motif
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Similarity 100.0%; Pred. No. 1.9e+02;
4; Conservative 0; Mismatches 0;
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C; Superfamily: regulatory protein P-II
                                                                                                               100.0%;
ilarity 100.0%;
Conservative 0
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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31 DYDA 34
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A; Gene: CAC0681
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F84355
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F87429
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C;Species: Listeria monocytogenes
C;Species: Reft.
D;Schaugez-Bernal, G; Duchaud, E; Durand, A; Baquero, F; Berche, P; Bloecker
D; Jones, L.M.; Karst, U
Science 294, 849-852, 2001
A;Authors: Kreft, J; Kuhn, M.; Kunst, F; Kurapkat, G; Madueno, E; Maitournam, A; Ma A;Authors: Kreft, J; Kunh, M.; Kunst, F; Kurapkat, G; Madueno, E; Maitournam, A; Maittle: Comparative genomics of Listeria species:
A;Title: Comparative genomics of Listeria species:
A;Status: preliminary
A;Residues: DNA
A;Residues: L-120 cGLA>
A;Cross-references: GB:NC_003210; PIDN:CAD01016.1; PID:g16412303; GSPDB:GN00177
A;Gene: Lmo2803
A;Gene: Lmo2803
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A;Molecule type: mRNA
                                                                                                                                                                  to Streptococcus pneu
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C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
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                                  C;Accession: D30540
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: D30540
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Pred. No. 2e+02;
Mismatches 0; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 100.0%;
Matches 4; Conservative 0;
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102 DYDA 105
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DYDA 61
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CiSpecies: Caulobacter crescentus
CiDate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
CiAccession: F87429
RiMierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelbe B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
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C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: F84355
R; Ng, W.V.; Rennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Largen, W.V.; Rennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Atlahors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T. A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-127 <STO>
A; Csoession: F8435
A; Residues: 1-127 <STO>
A; Csoession: GB:AE004437; NID:g10581477; FIDN:AAG20210.1; GSPDB:GN00138
C; Genetics:
A; Genetics:
A; Genetics:
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A; Molecule type: DNA
A; Residues: 1-124 <ST0>
A; Residues: 1-124 <ST0>
Cross-references: GB: AE005673; NID: 913422820; PIDN: AAK23434.1; GSPDB: GN00148
C; Genetics:
A; Gene: CC1453
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Length 121;
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                                                                      Indels
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Score 23; DB 2;
Pred. No. 2e+02;
                                                                   0; Mismatches
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Conserved hypothetical protein Atul327 [imported] - Agrobacterium tumefaciens (stracises: Agrobacterium tumefaciens c; Species: Agrobacterium tumefaciens c; Rocassion: Agrobact
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A,Reference number: AB2577; PMID:11743193
A,Accession: AG2739
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markel
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacteri
A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-132 <KUR>
A; Cross-references: GB:AE008688; PIDN:AAL42333.1; PID:g17739737; GSPDB:GN00186
A; Experimental source: strain C58 (Dupont)
C; Genetics:
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: E97520
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0;
              Pred. No. 2.2e+02;
Mismatches 0;
              Best Local Similarity 100.0%; P
Matches 4; Conservative 0;
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A;Molecule type: DNA
A;Residues: 1-132 <KUR>
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DYDA 127
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|DYDA 95
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F70659
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G.Species: Caulobacter crescentus
G.Species: Caulobacter crescentus
C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C.Accession: 687615
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter crescentus.
A.Accession: 687615
A.Reference number: A87249; MUID:21173698; PMID:11259647
A.Residues: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-129 <STO>
A.Cross-references: GB:AE005673; NID:913424591; PIDN:AAK24923.1; GSPDB:GN00148
G.Genetics:
A.Genetics:
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C;Species: Streptococcus pneumoniae
C;Daccession: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: B97875
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B97875
A;Andledule type: DMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 2; I ilarity 100.0%; Pred. No. 2.2e+02; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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|DYDA 40
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Nucleic Acids Res. 12, 6685-6700, 1984

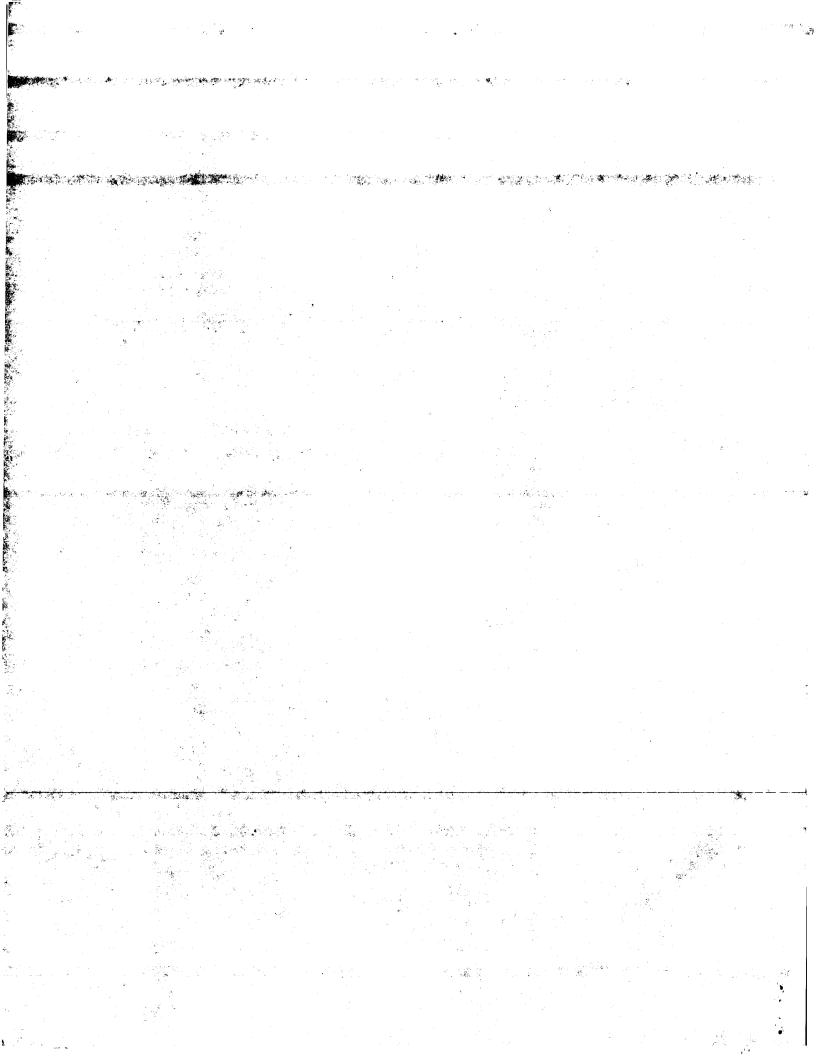
A;Title: Structural comparison of yeast ribosomal protein genes.
A;Reference number: A9332; MUID:85014125; PMID:6091033
A;Accession: A02820
A;Molecule type: DNA
A;Residues: 1-105, NIV. 113-142 < LEE>
A;Cross-references: EMBL:X01014; NID:944325; PIDN:CAA25506.1; PID:94326
B;Takahura, H.; Tsunasawa, S.; Miyagi, M.; Warner, J.R.
J. Biol. Chem. 267, 5442-5445, 1992
A;Title: NHZ-terminal acetylation of ribosomal proteins of Saccharomyces cerevisia
A;Reference number: S45500; MUID:92184799; PMID:1544921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-142 <ARI>
A;Residues: 1-142 <ARI>
A;Residues: 1-142 <ARI>
A;Cross-references: EMBL:274869; GSPDB:GN00015; MIPS:YOL127w; NID:g1420010; PIDN:CA;Experimental source: strain S288C
A;Experimental source: strain S288C
Yeast 12, 1013-1020, 1996
A;Title: Sequence analysis of a 13.4 kbp fragment from the left arm of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:U41293; NID:g1209710; PIDN:AAC49465.1; PID:g1209714
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1
C; Genetics:
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C; Species: Kluyveromyces marxianus
C; Species: Kluyveromyces marxianus
C; Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 13-Aug-1999
C; Accession: $30000
R; Bergkamp-Steffens, G.K.; Hoekstra, R.; Planta, R.J.
Yeast 8, 903-922, 1992
A; Title: Structural and putative regulatory sequences of Kluyveromyces ribosomal p
A; Reference number: $29999; MUID:93127726; PMID:1481569
A; Accession: $30000
A; Molecule type: DNA
A; Residues: 1-142 cABR>
A; Residues: 1-142 cABR>
A; Cross-references: GB:553422; NID:9263476; PIDN:AAB24897.1; PID:9263477
A; Note: the authors did not show the third nucleotide in the codon for 10-Ala
A; Gene: L25
A; Introns: 5/1
C; Genetics:
A; Genetics:
C; Superfamily: rat ribosomal protein L23a
C; Superfamily: rat ribosomal protein L23a
C; Keywords: protein biosynthesis; ribosome; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, submitted to the Protein Sequence Database, July 1996
A;Reference number: S66814
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C;Keywords: protein biosynthesis; ribosome; RNA binding
F;2-142/Product: ribosomal protein L23a.e #status experimental <MAT>
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N,Alternate names: ribosomal protein YL25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S71978; MUID:97051588; PMID:8896265
A; Accession: S71981
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llarity 100.0%; Pred. No. 2.4e+02;
Conservative 0; Mismatches 0;
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A;Cross-references: SGD:S0005487; MIPS:YOL127w
A;Map position: 15L
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A; Residues: 1-142 <CAW>
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Best Local Similarity
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129 DYDA 132
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C; Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70659
R;Cole, S.T.; Brosch, R.; Parkhill, J'; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-137 <COL>
A;Cross-references: GB:Z83863; GB:AL123456; NID:g3261685; PIDN:CAB06192.1; PID:e290871;
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams protein L23a.e, cytosolic - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein AOX142; protein 00534; protein YOL127w; ribosomal protein rg C;Species: Saccharomyces cerevisiae
S;Casamayor, A.; Khalid, H.; Balcells, L.; Aldea, M.; Casas, C.; Herrero, E.; Arino, J.
Submitted to the EMBL Data Library, November 1995
A;Description: Sequencing of a 13.4 kbp fragment of the left arm of chromosome XV reveal
A;Reference number: S63440
A;Reference number: S63440
A;Residues: 1-142 cAss
A;Residues: 1-142 cAss
A;Residues: 1-142 cAss
A;Cross-references: EMBL:U41293; NID:g1209710; PIDN:AAC49465.1; PID:g1209714
A;Experimental source: strain FY1679
R;Leer, R.J.; van Raamsdonk-Duin, M.M.C.; Hagendoorn, M.J.M.; Mager, W.H.; Planta, R.J.
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Search completed: February 6, 2003, 11:23:02 Job time : 14.5 secs



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3. /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1176, Ap Sequence 28253, A Sequence 28253, A Sequence 28253, A Sequence 27674, A Sequence 27674, A Sequence 1452, Ap Sequence 19310, A Sequence 19310, A Sequence 19310, A Sequence 19310, A Sequence 21054, A Sequence 21054, A Sequence 21054, A Sequence 21054, A Sequence 2121, App Sequence 121, App Sequence 121, App Sequence 122, App Sequence 123, App Description US-10-218-102-323 US-10-218-102-323 US-10-0274-1476 US-10-057-498-28553 US-10-092-411A-3420 PCT-USO2-3727-27674 US-10-057-498-27674 US-10-057-498-27674 US-10-513-999C-4805 US-09-513-999C-4805 US-09-513-999C-4805 US-10-513-999C-4805 US-10-513-999C-4805 US-10-513-99C-4805 US-10-057-498-13310 US-09-950-084-6433 PCT-USO2-3277-1054 US-10-194-975-121 US-10-319-763-120 PCT-USO2-22011-122 US-10-194-975-122 US-10-194-975-122 US-10-194-975-122 US-10-194-975-123 US-10-194-975-123 US-10-104-975-128 SUMMARIES DB Length Query Match 100.0 100.0 100.0 100.0 000 8 Score Result ģ

RESULT 2
US-10-276-774-1476
; Sequence 1476, Application US/10276774
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

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		-102-323 e 323, Application US/10 e NAT: Bentzien, Joerg ANT: Bahlyat, Bassil I. ANT: Dahlyat, Bassil I. ANT: Dahlyat, Bassil I. ANT: Dablyat, Bassil I. ANT: Hayes, Robert J. ANT: Hayes, Robert J. ANT: Vielmetter, Jost OF INVENTION: Protein De EFERENCE: A-67229-11/RET T FILING DATE: 2001-08-10 APPLICATION NUMBER: US 6 FILING DATE: 2001-09-10 APPLICATION NUMBER: US 6 FILING DATE: 2001-09-25 APPLICATION NUMBER: US 6 FILING DATE: 2001-09-25 APPLICATION NUMBER: US 6 FILING DATE: 2002-01-25 APPL	100.0%; 100.0%; ive
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		SULT 1 -10-218-102-323 Sequence 323, Applic, GENERAL INFORMATION: APPLICANT: Bentzien APPLICANT: Bentzien APPLICANT: Dasjarl APPLICANT: Hayes, APPLICANT: Hayes, APPLICANT: Hayes, APPLICANT: Vielmet, TITLE OF INVENTION: ELLE OF CURRENT APPLICATION CURRENT FILING DATE: PRIOR PILING DATE: PRIOR FILING DATE: PRIORALIFICITEMENT OTHER INFORMATION: -0.10-218-102-323	Ë,
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100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-498-28253
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Persing, David
Bhatia, Ajay
Maisonneuve, Jean Francois
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Jen, Shyian
Lodes, Michael
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 20121.51467
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 28253
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(58)
OTHER INFORMATION: Xaa = any amiņo acid or nothing
                                                                              FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
FRICR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SOFTWARE: CUSTOM
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OTHER INFORMATION: Xaa = Any Amino Acid
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US-10-057-498-28253
; Sequence 28253, Application US/10057498
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
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Jen, Shyian
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Matches 4; Conserv
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Matches 4; Conserv
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PCT-US02-32727-28253
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|DYDA 49
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20 DYDA 23
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APPLICANT:
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Sequence 5067, Application US/09513999C

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION:
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.022.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR PELLOR DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5667
LENGTH: 98
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GENERAL INFORMATION:
APPLICANT: LOGACH, MARTIN D.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 15966-543 CON
CURRENT APPLICATION NUMBER: US/10/218,140

CURRENT PILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 05/40,763
PRIOR APPLICATION NUMBER: 60/127,28

PRIOR APPLICATION NUMBER: 60/127,636

PRIOR FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 6322

SOFTWARE: CURANATOR VURSE: 60/127,607

PRIOR FILING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 6322

SOFTWARE: CURANATOR VERSION 1.0

SEQ ID NO 1452

LENGTH: 95
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  Length 94;
Score 23; DB 5; I
Pred. No. 1.8e+02;
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100.0%; Pred. No. 1.9e+02;
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llarity 100.0%; Pred. No: 1.9e+02;
Conservative 0; Mismatches 0;
                                          0; Mismatches
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Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
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; ORGANISM: Homo sapiens
US-09-513-999C-5067
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; ORGANISM: Homo sapiens
US-10-218-140-1452
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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US-09-513-999C-5067
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US-10-218-140-1452
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DYDA 81
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52 DYDA 55
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71 DYDA 74
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                                    APPLICANT: Carter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Barth, Brenda
APPLICANT: Bouglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
CURRENT PAPLICATION NUMBER: PCT/USO2/32727
CURRENT FILING DATE: 2002-10-11
SEQ ID NOS: 30992
LENGTH: 92
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Vasir
APPLICANT: Skeiky, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27674
LENGTH: 92
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Sequence 4805, Application US/09513999C

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPERBNCE: 59.US2.RES
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 4805

LENGTH: 94
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                      Jones, Robert
Carter, Darrick
Barth, Brenda
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  Benson, Darin
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; ORGANISM: Homo sapiens
US-09-513-999C-4805
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Best Local Similarity
4, Conserve
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Douglass, John Till Berling and Methods for the Therapy and Diagnosis of A TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 21054
LENGTH: 108
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APPLICANT: Karen J. Shaw TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods FILE REFERENCE: 1034/1C9639352 CURRENT APPLICATION NUMBER: US/09/950,084 CURRENT FILING DATE: 2001-09-10
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR PLING DATE: 1999-07-11
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR PELICATION NUMBER: US 09/266,555
PRIOR PELING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1999-03-10
PRIOR PLING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-06
REMAINING PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
REMAINING PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
REMAINING PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
REMAINING PRIOR APPLICATION NUMBER: US 09/036,750
PRIOR FILING DATE: 1998-03-06
REMAINING PRIOR PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
PRIOR PRIOR PRIOR APPLICATION DATE: 1998-03-06
PRIOR PRIOR PRIOR APPLICATION DATE: 1998-03-06
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Zhang, Yanni
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; ORGANISM: Staphylococcus aureus
US-09-950-084-6433
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Best Local Similarity 100.
Matches 4; Conservative
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Jen, Shyian
Lodes, Michael
Benson, Darin
Jones, Robert
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Barth, Brenda
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Bhatía, Ajay
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ORGANISM: Propioni acnes
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NAME/KEY: unsure
LOCATION: (2)
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PCT-US02-32727-21054
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36 DYDA 39
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APPLICANT:
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APPLICANT: Barth, Brenda
TITLE TOUGLASS John
TITLE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US/02/32727
CURRENT PILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
LENGTH: 99
TYPE: Carter Plant Pla
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Sequence 19310, Application US/1005/498

Sequence 19310, Application US/1005/498

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 21012.1.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
MUMBER OF SEQ ID NOS: 29212

LENGTH: 99
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Best Local Similarity 100.0%; Score 23; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
                                                                                          Sequence 19310, Application PC/TUS0232727 GENERAL INFORMATION:
                                                                                                                                                                                                                                        Persing, David
Bhatia, Ajay
Maisonneuve, Jean Francois
Zhang, Yanni
Wang, Siqing
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APPLICANT: George H. Shimer, Jr.
                                                                                                                                                                 APPLICANT: Mitcham, Jennifer APPLICANT: Skeiky, Yasir
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Best Local Similarity 100.
Matches 4; Conservative
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PCT-US02-32727-19310
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; ORGANISM: Propioni acnes
US-10-057-498-19310
                                                           PCT-US02-32727-19310
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US-09-950-084-6433
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54 DYDA 57
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54 DYDA 57
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APPLICANT:
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                   RESULT 11
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APPLICANT: BUGGLETT, Aymeric
APPLICANT: BOUGGLETT, Aymeric
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.USO4.DLV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/004,121
PRIOR APPLICATION NUMBER: 60/004,121
PRIOR APPLICATION NUMBER: 60/004,166
PRIOR PILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PLENT. PM
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US-10-319-763-120
US-10-319-763-120
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougleatet, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
                      TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 51371
                                                                                                                                                                                                                                                                            Score 23; DB 5; I
Pred. No. 2.3e+02;
; Mismatches 0;
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Pred. No. 2.3e+02;
Mismatches 0;
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ilarity 100.0%;
Conservative 0;
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; ORGANISM: Homo sapiens
US-09-724-676A-51371
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ORGANISM: Homo sapiens
        APPLICANT: Compugen LTD
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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US-10-319-763-214
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78 DYDA 81
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78 DYDA 81
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 21054
LENGTH: 108
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                                                                Query Match 100.0%; Score 23; DB 1; Length 108; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 23; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814. Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 51371
LENGTH: 114
; OTHER INFORMATION: Xaa - Any Amino Acid PCT-US02-32727-21054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: unsure
; LOCATION: (2)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-498-21054
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
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ORGANISM: Propioni acnes
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ORGANISM: Homo sapiens
US-09-724-676-51371
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US-09-724-676A-51371
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US-10-057-498-21054
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DYDA 81
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93 DYDA 96
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RESULT 23
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100.0%; Pred. No. 2.4e+02;
1ve 0; Mismatches 0;
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TITLE OF INVENTION: Super Humanized Antibodies
FILE REPERENCE: 50123.02
CURRENT APPLICATION NUMBER: PCT/US0/2/22011
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ. ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ. ID NO 121
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GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.02
CURRENT APPLICATION NUMBER: PCT/US02/22011
PRIOR APPLICATION NUMBER: US 60/305,111
                   CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
                                      CURRENT FILTING DATE: 200710/319,7

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR RILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121

PRIOR PILING DATE: 1998-02-09

PRIOR PILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-04-13

PRIOR PILING DATE: 1998-08-10

PRIOR PILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: 60/096,116

PRIOR PILING DATE: 1998-08-10

PRIOR PILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

NUMBER OF SEQ ID NOS: 229

SOFTWARE: PATCHL.PM
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; GENERAL INFORMATION:
REFERENCE: G-031.US04.DIV
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: -103..-1
US-10-319-763-120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Mus sp. PCT-US02-22011-121
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PCT-US02-22011-121
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; OTHER INFORMATION: humanized anti-human glutamic acid decaboxylase (GAD65) Fz ; OTHER INFORMATION: ent PCT-US02-22011-122
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FEATURE:
OTHER INFORMATION: humanized anti-human glutamic acid decaboxylase (GAD65) Fab
US-10-194-975-122
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GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 121
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GENERAL INFORMATION:
APPLICANT: Foote, Jefferson;
TITLE OF INVENTION: Super Humanized Antibodies;
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975;
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 122
LENGTH: 119
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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 122
LENGTH: 119
                                                                                               TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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Best Local Similarity 100.0
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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TYPE: PRT
ORGANISM: Mus sp.
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101 DYDA 104
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US-10-194-975-121
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skelky, Yasair
APPLICANT: Skelky, Tasair
APPLICANT: Skelky, Tasair
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of PITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of PITLE OF INVENTION: 2010:514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
SEQ ID NOS: 29212
LENGTH: 130
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FITLE OF INVENTION: Variants of alternative splicing
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 145
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 145
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                                        RESULT 26
8-10-057-498-5855
9-10-057-498-5855, Application US/10057498
GENERAL INFORMATION:
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CORGANISM: Propioni acnes
US-10-057-498-5855
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; ORGANISM: Homo sapiens
US-09-724-676-51020
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US-09-724-676A-51020
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36 DYDA 39
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US-10-264-237-1823
; Sequence 1823, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR PAPLICATION NUMBER: PCT/US01/16450
; PRIOR RELING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; NUMBER OF SEQ ID NOS: 2076
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NOS: 2076
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  Mismatches
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Malsonneuve, Jean Francois
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Benson, Darin
Jones, Robert
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Barth, Brenda
  Conservative
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Wang, Siqing
Jen, Shyian
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PCT-US02-32727-5855
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Matches 4; Conserv
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|DYDA 104
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39 DYDA 42
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36 DYDA 39
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PCT-US02-32727-23164
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US-10-057-498-23164
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| 157 DYDA 160
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                  LENGTH: 169
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APPLICANT:
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APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/12963US
CURRENT APPLICATION NUMBER: 08/09/950,084
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 08/09/35,718
PRIOR PLING DATE: 1999-10-14
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1998-03-10
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US-10-264-237-1916
Sequence 1916, Application US/10264237
Sequence 1916, Application US/10264237
Sequence 1916
TENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT FPLING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR PILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
WUMBER OF SEQ ID NOS: 2876
SOFTWARE: PATENTIN VET. 3.1
SEQ ID NO 1916
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                                        Indels
100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
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US-09-950-084-4003
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: George H. Shimer, Jr.
Best Local Similarity 100
Matches 4; Conservative
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Best Local Similarity 100.

Matches 4; Conservative
                                                                                                                                                 130 DYDA 133
                                                                                                                                                                                                                                       RESULT 29
US-09-950-084-4003
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APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 23164
LENGTH: 170
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVERTION: Compositions and Methods for the Therapy and Diagnosis of ACTIVE REFERENCE: 210121.314
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 23164
LENGTH: 170
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                                                                                        Query Match 100.0%; Score 23; DB 6; Length 169; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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; GENERAL INFORMATION:
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Bhatia, Ajay
Maisonneuve, Jean Francois
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Benson, Darin
Jones, Robert
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Barth, Brenda
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Wang, Siqing
Jen, Shyian
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ORGANISM: Propioni acnes
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1916
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Best Local Similarity
Matches 4; Conserv
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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-950-084-5911
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Best Local Similarity luv...
4; Conservative
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US-09-724-676-51015
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; ORGANISM: Homo sapiens
US-09-724-676A-51015
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserva
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160 DYDA 163
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66 DYDA 69
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GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Raren J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/12953US2
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
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SEQ ID NO 5911
LENGTH: 173
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                                                                                                                                                                         Sequence 2363.) Application US/10276774

GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
SOFTHAME: CURRENT FILING DATE: 2000-06-03
SOFTHAME: CURLENT ON NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
SOFTHAME: CURLENT ON NUMBER: 09/496,914
PRIOR 2363
LENGTH: 171
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PRIOR PELLING DATE: 1999-10-14
PRIOR PELLING DATE: 1999-10-14
PRIOR PELLING DATE: 1999-00-14
PRIOR PELLING DATE: 1999-07-14
PRIOR PELLING DATE: 1999-03-11
PRIOR PELLOATION NUMBER: US 09/266,555
PRIOR PELLING DATE: 1999-03-11
PRIOR PELLING DATE: 1999-03-10
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PRIOR PELLING DATE: 1998-03-06
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Best Local Similarity 100.
Matches 4; Conservative
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                                                               159 pypa 162
                                                                                                                                                        US-10-276-774-2363
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                     1 DYDA 4
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    Length 173;
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                                          Indels
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN version 3.2
SEQ ID NO 51015
LENGTH: 175
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Sequence 51015, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 51015
LENGTH: 175
Score 23; DB 5; ]
Pred. No. 3.5e+02;
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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100.0%; Score 23; DE ilarity 100.0%; Pred. No. 3.5 Conservative 0; Mismatches
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US-09-724-676-51015
IS-SEQUENCE 51015, Application US/09724676
GENERAL INFORMATION:
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30-09-950-084-3836
Sequence 3836, Application US/09950084
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
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FILE REFERENCE: 1034/1C963US2
CURRENT PAPPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR PILING DATE: 1999-10-14
PRIOR PELING DATE: 1999-07-14
PRIOR PELING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-10
PRIOR PELING DATE: 1999-03-10
PRIOR PELING DATE: 1999-03-10
PRIOR PELING DATE: 1998-03-06
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTENCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 418
LENGTH: 202
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100.0%; Score 23; DB 5; Length 202;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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US-09-134-000C-4718
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Best Local Similarity
Matches 4; Conserv
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US-09-134-000C-4718
; Sequence 4718, App
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88 DYDA 91
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BATECOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CORRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILDS PEPERANCE:
02796-032
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CURRENT APPLICATION NUMBER:
NUMBER OF SEQ ID NOS:
6012
SOFTWARE:
PARENT FILING DATE:
1997-08-13
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1997-08-13
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1997-08-15
NUMBER OF SEQ ID NOS:
6012
SOFTWARE:
1007-08-15
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BUREROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BURERS US/09/134,000C
TITLE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
LENGTH: 206
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100.0%; Pred. No. 4.2e+02;
ive 0; Mismatches 0;
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US-09-134-000C-3471
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GENERAL INFORMATION:
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US-09-134-000C-3471
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88 DYDA 91
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LENGTH: 202
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US-09-724-676-67070

Sequence 67070, Application US/09724676

GENERAL INFORMATION:
TILLE OF INVENTION: Variants of alternative splicing; TILLE OF INVENTION: Variants of alternative splicing; CURRENT APPLICATION NUMBER US/09/724,676

CURRENT FILING DATE: 2000-11-28

SOFTWARE: PATENTIN version 3.2

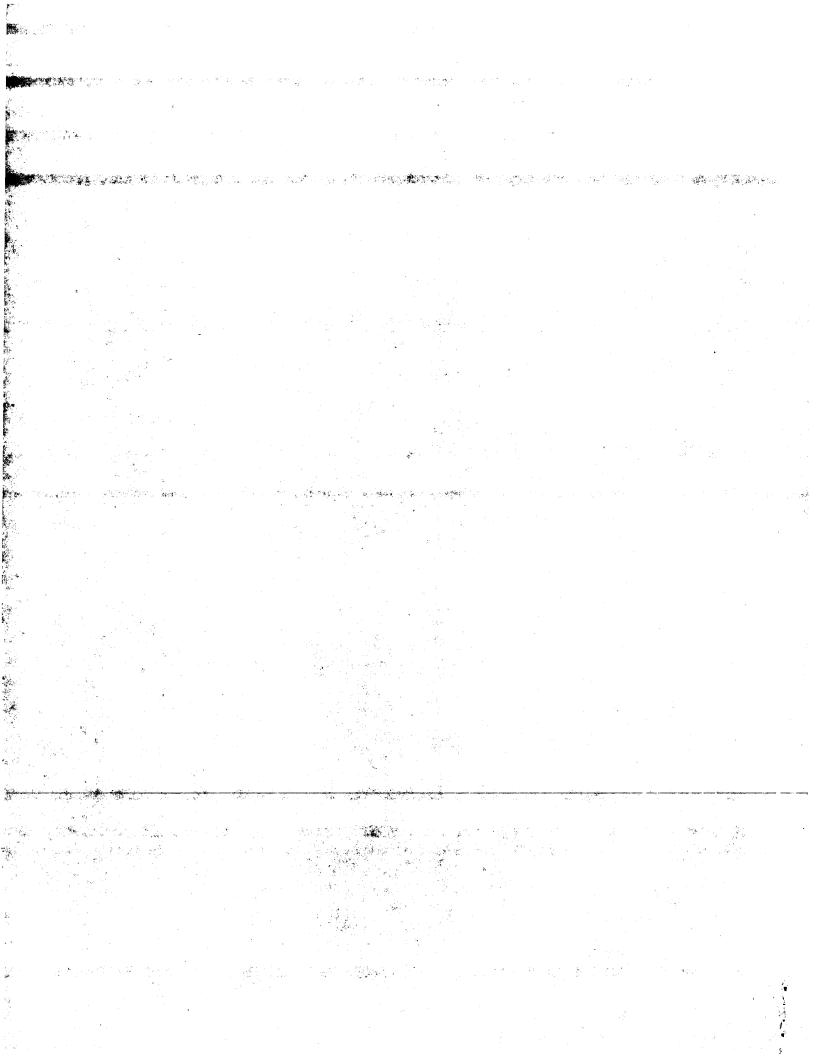
SEQ ID NO 6700

LENGTH: 225
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVERTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676
CURRENT FILNG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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Best Local Similarity 100.

Matches 4; Conservative
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US-09-724-676-67070
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              Query Match
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US-09-134-000C-3471
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US-09-724-676-67071
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US-09-724-676-67072
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Sequence 67073, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 225
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US-09-724-676-67072
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein . protein search, using sw model

February 6, 2003, 11:16:00 ; Search time 5.33333 Seconds
(without alignments)
31.107 Million cell updates/sec Run on:

PAT943-1 23 1 dyda 4

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	I31 MYCTU	O50386 mycoba	P80676	OLTU P58517 solanum t	P14109 bacterio	NASP 044149	007360 synechoco	075368	m smm 81j108 mns m	Q8y245			STRAL	AEEL Q9n2w7	CAEEL 020647	AEEL		XENLA	IXCTU Q10772	'RIAG 022644	RL2B_TOBAC Q07761 nicotiana	IUMAN P52298	JREPA 09pqi7	Q9kpu4	HUMAN P29316	DROME Q9nfp5	BACNO P27688	BACNO	MYCPN	P40019	BACNO P27689	
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P80676;
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STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
Stelstchmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn W.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE PHD/YEFM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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0
                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created) | 30-MAY-2000 (Rel. 39, Last sequence update) | 15-JUN-2002 (Rel. 41, Last annotation update) | 15-JUN-2002 (Rel. 41, Last annotation update) | RV3357 OR MT3465 OR MTV004.14.
                                                                                                                                                                                                                                                                      91 AA.
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Hvoothetical protein; Complete proteome.

And I0194 MW; 5A4140972F
     Pred. No.
                                                                                                                                                                                                                                                                   PRT;
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  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence.
                              Conservative
                                                                                                                                                                                                                                                                STANDARD;
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
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                                                                                                               DYDA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H37Rv
                                                                               1 DYDA 4
                                                                                                                                                                                                                                                                YX57_MYCTU 050386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYDA 4
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1111 DYDA 45

42

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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Blaberus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SERGING.

STRAIN-CV. Pentland squire; TISSUE-Tuber;

MEDLINE-92384955; Pubmed-1515078;

Strukelj B., Pungercar J., Mesko P., Barlic-Maganja D., Gubensek F., Kregar I., Turk V.;

Kregar I., Turk V.;

Kregar I., Turk V.;

Chan-dotelation of aspartic proteinase inhibitors from potato at the gene, CDNB and protein levels.";

Biol. Chem. Hoppe-Seyler 373:477-482[1992].

INHIBITING PROTEASES OF INVADING ORGANISMS (BY SIMILARITY).

SUBCELLUIAR LOCATION: Vacuolar (By similarity).

SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                  "Cuticular proteins from the giant cockroach, Blaberus craniifer."; Insect Biochem. Mol. Biol. 27:109-120(1997).
Structural protein; Cuticle; Repeat.
MOD_ERS 1 1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cuxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                   TISSUE=Polyric caeca;
MEDLINE=97218697; PubMed=9066121;
Jensen U.G., Rothmann A., Skou L., Andersen S.O., Roepstorff P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 99; 100.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE PROTEASE INHIBITOR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690142670EA491BB CRC64;
                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cuticle protein 2 (BC-NCP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JDN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease inhibitor 4 (PI-4) (Fragment)
    99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00452; STI; 1.
PROSITE; PS00283; SOYBEAN_KUNITZ; PARTIAL.
Serine protease inhibitor; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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PD000891; Kunitz_legume; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 AA; 9867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; S
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                        Blaberus craniifer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 4; Conserv
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pat943-1.rsp

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NIFW_SYNP8
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    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                        Gaps
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  REACTIVE BOND (FOR CHYMOTRYPSIN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
P22-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kropinski A.M.B., VanderByl C.S.;
"The completed sequence of genome of Salmonella phage P22.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBU databases.
-!- FUNCTION: IN THE ABSENCE OF GP17, P22 IS SENSITIVE O A
SUPERINFECTION EXCLUSION SYSTEM OF THE FEL-2 PROPHAGE.
                                                                                               Score 23; DB 1; Length 103;
Pred. No. 72;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 1; Length 103; Pred. No. 72; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89293845; PubMed-2738922;
Semerijan A.V., Malloy D.C., Poteete A.R.;
"Genetic structure of the bacteriophage P22 PL operon.";
J. Mol. Biol. 207:1-13(1989).
                                       BY SIMILARITY.
D328692B166B21C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 AA; 12184 MW; ABD1224712320E2C CRC64;
                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Superinfection exclusion protein (Protein gpl7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitrogenase stabilizing/protective protein nifw.
NIFW OR ALL1433.
                                                                                                                                                                                                                                                                                                                   103 AA.
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                      SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC 7120)
                                       73 B
11349 MW;
                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
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                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                   STANDARD;
56
                                                       103 AA;
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Best Local Similarity
                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage P22
25
                                       26
                                                                                                                                                                                                    11 DYDA 20
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                                                                                                                                                                             1 DYDA 4
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P14109;
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Q44149;
                                     DISULFID
ACT_SITE
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VG17_BPP22
AC 01-JAN.
DT 01-JAN.
DT 01-JAN.
DT 16-OTAN.
DE SUPERTIJ
ON NCBL 17.
O
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                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-!- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99231861; PubMed=10217509;
Huang T.-C., Lin R.-F., Chu M.-K., Chen H.-M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain RF-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - 1- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bacteria; Cyanobacteria; Chrococcales; Cyanothece.
                                                                                                                                                                                                                                               MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Homotrimer, associates with nifD (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                damage (By similarity).
-!- SUBUNIT: Homotrimer; associates with nifb (By similarity).
-!- SIMILARITY: BELONGS TO THE NIFW FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                          Buikema W.J., Scappino L.A., Haselkorn R.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
12262 MW; 498DF9B8ADB8B95F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sennotation update)
Nitrogenase stabilizing/protective protein nifw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; 100.0%; Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U47055; AAA87952.1; -. EMBL; AP003585; BAB73390.1; InterPro; IPR004893; Nifw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       damage (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03206; NifW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitrogen fixation;
SEQUENCE 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 4; Conserv
                                                                                                FROM N.A.
                                 NCBI_TaxID-103690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111
24 DYDA 27
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007360;
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Thu Feb

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egeo A., Mazzocco M., Arrigo P., Vidal-Taboada J.M., Oliva R., Piroda B., Giglio S., Rasore-Quartino A., Scartezzini P.; "Identification and characterization of a new human gene encoding small protein with high homology to the proline-rich region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                        Score 23; DB 1; Length 111; Pred. No. 78; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; Length 114; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. --- TISSUE SPECIFICITY: UBIQUITOUS. --- SIMILARITY: BELONGS TO THE SH3BGR FAMILY.
                                                                                                                                                                           111 AA; 12931 MW; C85B39697EFC310E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D72AC2A095F1AA8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SH3 domain-binding glutamic acid-rich-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 247:302-306(1998).
                                                                                                                                                                                                                                                                                                                                                                                    114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
MEDLINE=98308110; PubMed=9642120;
                                                                                                         EMBL; AF003700; AAC35197.1; -. InterPro; IPR004893; NifW. Pfam; PF03206; NifW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF042081; AAC27445.1; -. EMBL; BC016709; AAH16709.1; -.
                                                                                                                                                                                                        100.0%;
100.0%;
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Similarity 100.0%;
4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:10823; SH3BGRL.
MIM; 300190; -.
                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 114 AA;
                                                                                                                                                            Nitrogen fixation.
                                                                                                                                                                                                                       Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                         |||||
DYDA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3-binding.
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                                                                                                                                                                                                                                                                                                                                                                                  SH3L_HUMAN
075368;
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3BGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3BGR
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Matches
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                                                                                                                                                                                                                                                                                                      27
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1 DYDA 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Bilault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Squisr P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 1; Length 114; 100.0%; Pred. No. 80; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           Scartezzini P., Egeo A., Mazzocco M.; "Cloning the mouse homolog of the human SH3BGRL gene."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.!- SIMILARITY: BELONGS TO THE SH3BGR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH3-BINDING (POTENTIAL).
D7298AF8F5BFA43F CRC64;
                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SH3 domain-binding glutamic acid-rich-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein 89.
                                                                                   114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 AA.
                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GMI1000;
MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ272504; CAB76919.1; -. MGD; MGI:1930849; Sh3bgrl.
                                                                                                                    16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 AA; 12811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30S ribosomal protein S9. RPSI OR RSC0491 OR RS05034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
DYDA 81
                                                                             SH3L_MOUSE
Q9JJU8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 DYDA 81
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                                                                                                                                                                                      SH3BGRL.
                                                                   SH3L_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
78
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                                               RESULT 9
g
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STRAIN=S288C / FY1679;
MEDLINE=97051588; PubMed=8896265;
Casamayor A., Khalid H., Balcells L., Aldea M., Casas C.,
Herrero E., Arino J.;
"Sequence analysis of a 13.4 kbp fragment from the left arm of chromosome XV reveals a malate dehydrogenase gene, a putative Ser/Thr protein kinase, the ribosomal L25 gene and four new open reading
                                                             Leer R.J., van Raamsdonk-Duin M.M.C., Hagendoorn M.J.M., Mager W.H.,
Planta R.J.;
                                                                                 Planta R.J.; "Structural comparison of yeast ribosomal protein genes.";
                                                                                                     Nucleic Acids Res. 12:6685-6700(1984)
                                                                                                                                                                                                                                                                          SEQUENCE OF 1-20.
MEDLINE=92184799; PubMed=1544921;
                                        STRAIN=Carlsbergensis;
MEDLINE-85014125; PubMed-6091033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U41293; AAC49465.1; -. EMBL; X01014; CAA25506.1; -. EMBL; Z74869; CAA99146.1; -. PIR; AO2820; R58Y25.
                                                                                                                                                                                                                                                 Yeast 12:1013-1020(1996)
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es 4; Conserv
                                                                                                                               SEQUENCE FROM N.A.
  NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                cerevisiae.
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Q53595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                        frames.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-79148387; PubMed=107028;
Dhaese P., Vandekerckhove J., van Montagu M.;
The primary structure of the coat protein of the broad-host-range
TNA bacteriophage PRR1.';
Eur. J. Biochem. 94:375-386(1979).
-!-FUNCTION: FORMS THE PHAGE SHELL; BINDS TO THE PHAGE RNA.
InterPro; IPR002703; Levi_coat.
PIRs, P04225; VGBPR1.
InterPro; IPR002703; Levi_coat.
Pfam, PF01819; Levi_coat.
SEQUENCE 131 AA; 14535 MW; E7E639E1E50FC612 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae; NCBL_TaxID=12024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
60S ribosomal protein L25 (YL25) (RP6LL).
SPL25 OR YOL127W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
 -! - SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                       Score 23; DB 1; Length 130;
Pred. No. 92;
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Pred. No. 93;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                               Ribosomal protein; Complete proteome.
SEQUENCE 130 AA; 14336 MW; A539A49A953DE1A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   131 AA
                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                       InterPro; IPR000754; Ribosomal_S9.
Pfam; PF00380; Ribosomal_S9; 1.
PROSITE; PS00360; RIBOSOMAL_S9; 1.
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                                                                                                                              EMBL; AL646059; CAD14019.1; -.
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100.0%;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein.
Bacteriophage PRR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                  89 DYDA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 DYDA 95
                                                                                                                                                                                                                                                                          1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                   COAT_BPPRR
P03616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RL25_YEAST
P04456;
                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                         RESULT 11
COAT_BPPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
RL25_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                   J. Biol. Chem. 267:5442-5445(1992).
-!- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC REGION ON THE 26S RRNA.
-!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces albus G.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
"NH2-terminal acetylation of ribosomal proteins of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVLKVNT -> NI (IN REF. 1)
C53ED3DA4A9D219A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 1; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 37, Last annotation update)
shock protein (HSP 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proben Proposition (1978) Proposition (1978) Proposition (1978) Probom: Probom: Probom: Probom: Probom: Proposition (1978) Prostre: Psonoso; RIBOSOMAL_L33; 1. PROSTRE: PSONOSO; RIBOSOMAL_L33; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein; rRNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 AA; 15626 MW;
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pat943-1.rsp

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F52B5.6
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RL2C_CAEEL
                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0UN-2002 (Rel. 41, Last annotation update)
Putative NADH-ubiquinone oxidoreductase subunit B17.2 (EC 1.6.3)
(EC 1.6.99.3) (Complex I-B17.2) (CI-B17.2).
                                             Servant P., Mazodier P.; "Characterization of Streptomyces albus 18-kilodalton heat shock-
                                                                      responsive protein.";
J. Bacteriol. 177:2998-3003(1995).
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
-- FAMILY.
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                        Score 23; DB 1; Length 143;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                 143 AA; 16107 MW; DCB8FA0DE154B197 CRC64;
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                   MEDLINE=95286476; PubMed=7768794;
                       SEQUENCE FROM N.A., AND PARTIAL
                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
                                                                                                                                                                                                                                     EMBL; U17419; AAA86472.1; -. InterPro; IPR002068; Hsp20. Pfam; PF00011; HSP20; 1. PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity).
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
 NCBI_TaxID=1962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                            109 DYDA 112
                                                                                                                                                                                                                                                                                                                                                                      1 DYDA 4
                                                                                                                                                                                                                                                                                      Heat shock
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          N7BM_CAEEL
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EMBL; AC024876; AAF60889.1; ALT_INIT.
WORMPep; Y94H6A.8; CE25630.
Hypothetical protein; Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 146 AA; 17073 MW; 0A8549D622977786 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kershaw J.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC REGION ON THE 26S RRNA
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                              Length 146;
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Ribosomal protein; rRNA-binding.
SEQUENCE 146 AA; 16283 MW; 3380545260EA88C7 CRC64;
                                                                                                                                                                                                                     Score 23; DB 1; I
Pred. No. 1.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.1e+02;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable 60S ribosomal protein L23A 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
RIZB_CAREL

AC PULSB_CAREL

AC PAR162;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DF 01-FEB-1996 (Rel. 33, Last sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormPep; F52B5.6; CE05721.
InterPro; IPR001014; Ribosomal_L23.
                                                                                                                                                                                                                         100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 DYDA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 DYDA 136
                                                                                                                                                                                                                                                                                                                                                                                         1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL2C_CAEEL
Q20647;
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1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
  SERBERRES
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                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ArCC 43067;

STRAIN-JAL-1 / DSM 2661 / ArCC 43067;

MEDLINE-9633999; Pubmed-8680887;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

'Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 1; Length 147; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probon: PD001141; Ribosomal_L23; 1.
PROSITE; PS00050; RIBOSOMAL_L23; 1.
Ribosomal protein: rRNA-binding.
SEQUENCE 147 AA; 16696 MW; 1F3FF0088C453955 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1- SIMILARITY: STRONG, TO M.JANNASCHII MJ0605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                WormPep; F55D10.2; CE02777.
InterPro; IPR001014; Ribosomal_L23.
Pfam; PF00276; Ribosomal_L23; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U40948; AAA81728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein MJ0142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                          SIMILARITY).
                                                        SEQUENCE FROM N.A. STRAIN-Bristol N2;
                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 DYDA 137
                                                                                             Leimbach D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y142_METJA
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Y142_METJA
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                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Kidney epithelium;
MEDLINE-95379956; Pubmed--651522;
Izaurralde E.L., Lewis J., Gamberi C., Jarmolowski A.,
McGulgan C., Mattal J. W.;
A cap-binding protein complex mediating U snRNA export.";
Nature 376:709-712(1995).
-! FUNDTION: INVOLVED IN MEDIATING U SNRNA EXPORT FROM THE NUCLEUS.
-! SUBUNIT: THE CAP-BINDING PROTEIN (CBC) COMPLEX IS AN HETERODIMER
OF CEPRO AND CEP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
20 kDa nuclear cap binding protein (NCBP) (CBP20) (Fragment).
                                                                                                                                                                                                                                                         Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 148;
                                                                                                                                                                                                                                 Score 23; DB 1; Length 14
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-BINDING (RRM).
007CDACABDC89A8C CRC64;
                                                                                                                                                                                                        707D67BF058E065C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
or send an email to license@isb-sib.ch).
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Ffam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS001030; RRM_RNP_1; FALSE_NEG.
Nuclear protein; RNA-binding.
                                                                                                                                                                                                                                                         100.0%; Sci
100.0%; Pr
tive 0;
                                                                                           InterPro; IPR002806; DUF103.
Pfam; PF01953; DUF103; 1.
Probom; PD015886; DUF103; 1.
Hypothetical protein; Complete SEQUENCE 147 AA; 17592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
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                                                  EMBL; U67471; AAB98125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X84788; CAA59259.1;
HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                               102 DYDA 105
                                                                                                                                                                                                                                                                                                                                                                 1 DYDA 4
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P52299;
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pat943-1.rsp

154 AA

STANDARD;

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15-JUL-1998 (Rel. 36, Created)
                                                                                           15-JUL-1998
15-JUL-1998
                  RL2B_FRIAG
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RL2B_TOBAC
                ALD DE STORY OF STORY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-9825987; PubMed-9634230; Garnier T., Churcher C., Harris D., Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Egilmeler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Gquares S., Squares R., Selton J.E., Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO M.TUBERCULOSIS, RV1261C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 protein; Complete proteome.
148 AA: 16347 MW; A9F98E90398719B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; L
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created) | 01-0CT-1996 (Rel. 34, Last sequence update) | 15-JUN-2002 (Rel. 41, Last annotation update) | 19-pothetical protein RV1558 OR MT1609 OR MTCY48.07C.
                                                                                                                                                             148 AA
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TubercuList; Rv1558; -...
Interpro; IPR004378; Mtu_fam_11.
TIGRRAMS; TIGRO0005; Mtu_fam_11; 1.
Hypothetical protein; Complete prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE007027; AAK45876.1; -.
                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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Query Match
Best Local Similarity 100...
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                                                                                                                                                           STANDARD;
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SEQUENCE FROM N.A.
1111
133 DYDA 136
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                                                                                                                                                     YF58_MYCTU
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                                                                                                     RESULT 19
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100 DYDA 103

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RESULT 20 RL2B_FRIAG

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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Prabhavalkar D.S., Baysdorfer C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC REGION ON THE 26S RRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 25:761-770(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=94355650; PubMed=8075394;
Gao J., Kim S.R., Chung Y.Y., Lee J.M., An G.;
"Developmental and environmental regulation of two ribosomal protein
                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Liliales; Liliaceae;
Fritillaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-OCT-1994 (Rel. 30, Last sequence update)
O1-FEB-1996 (Rel. 33, Last annotation update)
60S ribosomal protein L23A (L25).
RPL23A OR RPL25.
Nicotiana tabacum (Common tobacco).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
NUBI_TAXID=4097;
                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probon: PD00141; Pibosomal_L23; 1.
PROSITE; PS00050; RIBOSOWAL_L23; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 154 AA; 17350 MW; 5252CE2D969A52F CRC64;
      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last seqn
01-FEB-1996 (Rel. 33, Last anno
                                            60S ribosomal protein L23A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.00
-has 4; Conservative
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(Rel. 36, (Rel. 36,
                                                                                   Fritillaria agrestis.
                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
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                                                                                                                                                                              NCBI_TaxID=64177;
                         (Rel
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007761;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
20 kba nuclear cap binding protein (NCBP 20 kba subunit) (CBP20) (NCBP 11nteracting protein 1) (NIP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN MEDIATING U SNRNA EXPORT FROM THE NUCLEUS.
BINDS TO 5'CAPPED MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kataoka N., Ohno M., Moda I., Shimura Y.;
"Identification of the factors that interact with NCBP, an 80 kDa
nuclear cap binding protein.";
Nucleic Acids Res. 23:3638-3641(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 154; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A cap-binding protein complex mediating U snRNA export."; Nature 376:709-712(1995).
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-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                              84A845DF1161067E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 9-25 AND 113-145. MEDLINE-95379956; PubMed-7651522; Izaurralde E., Lewis J., Gamberi C., Jarmolowski A., McGuigan C., Mattaj A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AA.
                                                                                                                                                                                           InterPro; IPR001014; Ribosomal_L23.
Pfam; PF00276; Ribosomal_L23; 1.
PROSUTE; P0001141; Ribosomal_L23; 1.
PROSITE; PS00050; RIBOSOMAL_L23; 1.
Stibosomal protein; rRNA binding.
SEQUENCE 154 AA; 17281 MW; 84A84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Cervical carcinoma;
MEDLINE-96017765; PubMed-7478990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X84157; CAA58962.1; -. EMBL; D59253; BAA09599.1; -.
                                                                                                                                                                EMBL; L18908; AAA53296.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity الاست
الا Conservative با
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB20_HUMAN
P52298; Q14924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE-Cervix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 DYDA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
CB20_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HID DESCRIPTION OF COLUCTOR STREET ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPRO1437; GreA_GreB.
Pfam; PF01272; GreA_GreB. 1.
Pfam; PF01249; GreA_GreB. 1.
Probom; P00449; GreA_GreB.; 1.
PROSITE; PS00829; GREAB_1; 1.
PROSITE; PS00830; GREAB_1; 1.
Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
DOMAIN 7 24 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 4(7):157-762(2000).

Nature 4(7):157-762(2000).

-1- FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION

ELONGATION FAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING

SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION

OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN

LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY

CLEAVAGE FACTORS SUCH AS GREA OR GREB ALLOWS THE RESUMPTION OF

ELONGATION FROM THE NEW 3'TERNINUS. GREA RELEASES SEQUENCES OF

2 TO 3 NUCLEOTIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                  A -> S (IN REF. 2).
B6C94F3182A2CC3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 1; L
100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                       RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA.
                                                                             Interpro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS00102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Nuclear protein; RNA_binding.
DOMAIN
40 118 RNA-BINDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Serovar 3; MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE002128; AAF30713.1; -. HSSP; P21346; 1GRJ.
                                                                                                                                                                                                                                                                                                                           18001 MW;
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
HSSP; P11940; 1CVJ.
Genew; HGNC:7659; NCBP2.
                                                                                                                                                                                                                                                                                                                              156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 DYDA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GREA OR UU304
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                                                                 MIM; 605133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GREA_UREPA
                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GREA_UREPA
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72 DYDA 75

1 DYDA 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20406833; PubMed=10952301;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000).

I PENCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribity1-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethy1-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribity1-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethy1-8-lumazine (By similarity).

I-CARALYTIC ACTIVITY: 2 6,7-dimethy1-8-(1-D-ribity1)lumazine = riboflavin + 4-(1-D-ribity1amino)-5-amino-2,6-dihydroxypyrimidine.

I-PATHWAY: Riboflavin blosynthesis; last step.
                                                                                         Gaps
                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created) | 16-OCT-2001 (Rel. 40, Last sequence update) | 15-UN-2002 (Rel. 41, Last annotation update) | 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase) (Lumazine synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                       0
                                                       Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 156;
                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COIL (POTENTIAL).
86BEA8EC07C96461 CRC64;
                                                   Score 23; DB 1; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 1; L. Pred. No. 1.1e+02; Mismatches 0;
                                                                                                                                                                                                                                     156 AA
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004298; AAF95412.1; ALT_INIT.
HSSP; P11998; 1RVV.
TIGR; VC2268; -
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002180; DMRL_synthase. Pfam; PF00885; DMRL_synthase; 1. ProDom; PD003664; DMRL_synthase; 1.
                                                                                0;
 84 CC
17767 MW;
                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                   100.0%;
                                                                                4; Conservative
                                                                                                                                                                                                                                   STANDARD;
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Riboflavin biosynthesis;
               156 AA;
                                           Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                 VC2268
                                                                                                                                               47 DYDA 50
                                                                                                                 1 DYDA 4
                                                                                                                                                                                                                               RISB_VIBCH
Q9KPU4;
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
                                                                                                                                                                                                                                                                                                                                                 RIBH OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                               Matches
                                                                                                                                                                                                  RESULT
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"The primary structure of rat ribosomal protein L23a. The application of homology search to the identification of genes for mammalian and yeast ribosomal proteins and a correlation of rat and yeast ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 268:2755-2761(1993).
-!- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC REGION ON THE 26S RRNA
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fan W., Cai W., Parimoo S., Lennon G.G., Weissman S.M.;
"Identification of seven new human MHC class I region genes around
"Incompared to the control of the
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-Human;
MEDLINE=98086480; PubMed=9417910;
Fan W., Christensen M., Eichler E., Zhang X., Lennon G.;
"Cloning, sequencing, gene organization, and localization of human ribosomal protein RPL23A gene.";
Genomics 46:234-239(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Human; TISSUE-Melanoma;
Jiang H., Lin J., Tao J., Fisher P.B.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reddy K.B., Lin C.W., Howe P.H.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo M., Soares M.B.;
Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Rat; STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-93155091; PubMed-8428950;
Suzuki K., Wool I.G.;
                        HUMAN SIGN...
RE2B_HUMAN SIGN...
P29316; P39024; Q92774;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
TWN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96269983; PubMed=8662070;
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606, 10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunogenetics 44:97-103(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-Human; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES=Mouse; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 10-156 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Skin;
                                                                                                                                                                                                                                                                                             (Mouse), and
                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the HLA-F locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                          musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins.'
                           RL2B_HUMAN
RESULT 25
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Gaps

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Indels

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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley;

MEDLINE-20196006; PubMed-10731132;

Adman M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota; Merazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
-1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH3B_DROWE STANDARD; PRT; 158 AA.
09NFP5; 09VS88;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SH3 domain-binding glutamic acid-rich protein homolog (SH3BGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; Length 156; Pred. No. 1.1e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K -> N (IN REF. 3).
K -> S (IN REF. 3).
3980E77B47FAB70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MA -> IP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00276; Ribosomal_L23; Drobom; PD001141; Ribosomal_L23; DROSITE; PS00050; RIBOSOMAL_L23; DRIBOSOMAL_L23; DRIBOSOMAL_L23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR001014; Ribosomal_L23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC029992; AAH29892.1; --
EMBL; X65228; CAA46336.1; --
EMBL; X65228; CAA46336.1; --
PIR; A45214; A45214.
SWISS-2DPAGE; P29316; HUMAN.
Genew; HGNC:10317; RPL23A.
                                                                                                                                                                                                                                                                                                                                        U02032; AAA03341.1; -. U37230; AAB17510.1; -. AF001689; AAC51934.1; -. BC014459; AAH14459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                          EMBL; U43701; AAB03210.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L13799; AAA35681.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein).
SH3BGR OR CG8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 DYDA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; I
EMBL; I
EMBL; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
SH3B_DROME
                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Becker A., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotchar P., Brotchan B.S., Borkova D., Brotchar P., Bouck J., Brokstein P., Brotchar B., Brotchar J., Cadieu E., Center A., Chandra I., R. Dedson K., Deug J., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borsler C., Gabriellan A.E., Garrell J.H., Gu Z., Guan P., Harris M., Glasser K., A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Andrew D., Heiman T.J., Hernandez J.R., Houck J., Basto P., Lei Y., Howland T.J., Hernandez J.R., Houck J., A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kendson J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kendson J., Lai Z., Liang Y., Lin X., Andtei B., McIntosh T.C., McLeod M.P., Moshrefi A., Shen H., Shen Kimmel D.R., Sander E., Scheler E., Shen H., Shen B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., Shen R., Wassarman D.A., Weinstock G.M., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wang S., Zhu X., Smith H.O., Rang R. W. R., Sheng S., Yen S., Zhu X., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CAUTION: Ref. 2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Last annotation update) Fimbrial protein precursor (Pilin) (Serogroup B1/AC20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9DEF79C3D48CA463 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NK -> LL (IN REF. 1).
QQ -> HE (IN REF. 1).
D -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE SH3BGR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteroides nodosus (Dichelobacter nodosus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ272505; CAB76915.1; -.
EMBL; AE003559; AAF50570.1; ALT_SEQ.
FlyBase; FBgn0035772; CG8582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 23, Created)
(Rel. 23, Last sequ
(Rel. 23, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene model prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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13
20
64
158 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992
01-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
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GREA_MYCPN
P78019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae.
                                                                                                                                                                                                                                                                                        RESULT 29
GREA_MYCPN
     δλ
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         ö
                                       Gaps
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 1; Length 160; 100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                    FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY).
55ABC905E5B5057C CRC64;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Fimbrial protein precursor (Pilin) (Serogroup B1/AC127).
                                                                                                                             SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  160 AA.
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                         Pfam; PF00114; pilin; 1.
Prochom; Pp000066; pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
Fimbria; Methylation.
                                                                                                                                                                                                                               HSSP; P02974; ZPIL.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                     160 AA; 16693 MW;
                                                                                                                                                                                                                EMBL; M37473; AAA23338.1; -. PIR; PS0420; PS0420.
                                                                                                                                                                                                                                                                                                                          Query Match
Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                    160
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                 NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dichelobacter
                                                                                                                                                                                                                                                                                                                                                                                |||||
91 DYDA 94
                                                                                                                                                                                                                                                                                                                                                                       1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                               FMA7_BACNO P27691;
                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                    CHAIN
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FMA7_BACNO
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the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUGCIEC ACIGS RES. 24:4420-4449(1996).

**INCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION ELONGATION PAGT TEMPLATE-ENCODED ARRESTING STIES. THE ARRESTING STIES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY CLEAVAGE FACTORS SUCH AS GREA OR GREB ALLOWS THE RESUMPTION OF ELONGATION FROM THE NEW 3'TERMINUS. GREA RELEASES SEQUENCES OF 2 TO 3 NUCLEOTIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; Pubmed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHYLATION (BY SIMILARITY).
7CBC909FF48287AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            fam; PF00114; pilin; 1.
Probom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
Fimbria; Methylation.
                                                                                                                                                                                                                                                                                                                                                        HSSP, P02974; IAY2.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 AA; 16674 MW;
                                                                                                                                                                                                                                                                                                 EMBL; M37472; AAA23340.1; -. PIR; PS0419; PS0419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GREA OR MPN401 OR MP437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2104;
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91 DYDA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DYDA 4
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MOD_RES
SEQUENCE
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NCBI_TaxID=870;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GREA_MYCGE
P47524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GREA_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aatches
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                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Hyman R., Rayser A., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wel Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DbBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
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                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 18.3 kDa protein in GALB3-YPTB intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; Length 160; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                      Score 23; DB 1; Length 160; Pred. No. 1.2e+02; 0; Mismatches 0; Indels
                                                                                        Transcription regulation; DNA binding; Coiled coil; Con DOMAIN 8 28 COILED COIL (POTENTIAL). DOMAIN 48 75 COILED COIL (POTENTIAL). SEQUENCE 160 AA; 18101 MW; 32448C91712A19C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein.
160 AA; 18306 MW; 86BBE29FFE3D948B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AA.
                                                                                                                                                                                                                                                                                     160 AA
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        HSSP; P21346; IGRJ.
InterPro; IPR001437; GreA_GreB.
Pfam; PF01272; GreA_GreB; 1.
Pfam; PF03449; GreA_GreB_N; 1.
ProDom; PD00491B; GreA_GreB_N; 1.
PROSITE; PS00839; GRERB_L; 1.
PROSITE; PS00830; GREAB_Z; 1.
 EMBL; AE000043; AAB96085.1; -.
                                                                                                                                                     100.08;
                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U18778; AAB64563.1; -. SGD; S0000832; YER030W.
                                                                                                                                                                Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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49 DYDA 52
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P27689;
                                                                                                                                                                                                                                                                                     YEMO_YEAST
                                                                                                                                                      Query Match
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FMA3_BACNO
                                                                                                                                                                                                                                                                                                 P40019
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YEMO_YEAST
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                                                                                                                                                                                                                                                                           Gaps
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STRAINS-ATCC 33530 / G-37;
STRAINS-GO26346; PubMed-7569993;
MEDLINE-96026346; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                המנונים ומספס (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY).
3F0CF00DBF9EA385 CRC64;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Fimbrial protein precursor (Pillin) (Serogroup B1/AC293).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 1; 1
100.0%; Pred. No. 1.2e+02;
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Probom; PP00066; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
Fimbria; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M37474; AAA23339.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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Les 4; Conserv
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; DNA-binding; Coiled coil; Complete proteome. BOMAIN 9 28 COLLED COIL (POTENTIAL). DOMAIN 47 76 COILED COIL (POTENTIAL). SEQUENCE 161 AA; 18162 MW; 67E2850CB59BCC5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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"Nucleotide sequence of the Streptococcus gordonii PK488
coaggregation adhesin gene, scaA, and ATP-binding cassette.";
Infect. Immun. 62:4469-4480(1994).
-!-FUNCTION: HAS ANTIOXIDANT ACTIVITY. COULD REMOVE PEROXIDES
H(2)O(2) (BY SIMILARITY).
-!-SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TPX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%; Score 23; DB 1; Length 161; Local Similarity 100.0%; Pred. No. 1.2e+02; les 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Probable thiol peroxidase (EC 1.11.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD004918; GreA_GreB; 1.
PROSITE; PS00829; GREAB_1; 1.
PROSITE; PS00830; GREAB_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95012638; PubMed=7927711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interproj IPR001437; Grea_GreB. Pfam; PF01272; Grea_GreB. 1. Pfam; PF03449; Grea_GreB_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN 47 76 SEQUENCE 161 AA; 18162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus gordonii Challis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39708; AAC71504.1; -. HSSP; P21346; 1GRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 DYDA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGR; MG282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PK488
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P42366;
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Matches
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        RAPA RAPA PARAPA PARAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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     EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 162; 100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
  and the
                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                            B49E665E238C7484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA; 17754 MW; B48F965E238C7484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; I
Pred. No. 1.2e+02;
0; Mismatches 0;
 the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Probable thiol peroxidase (EC 1.11.1..).
                                                                                                                                                                                                                                                                                                                                                                               162 AA
                                                                                                                                                                                                                              100.0%; Pred. No.
                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91147187; PubMed=1671775;
                                                                                          EMBL; L11577; AAA71948.1; -.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR002065; TPX.
Pfam; PF00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
                                                                                                                                                                                            162 AA; 17781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000866; AhpC-TSA.
InterPro; IPR002065; TPX.
Pfam; PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100.0%; 4; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M63481; AAC98427.1; -.
                                                                                                                                                                Oxidoreductase; Peroxidase. INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; Proco.,
PROSITE; PS01265; TPX; 1.
Oxidoreductase; Peroxidase.
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sanguis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; B43583; B43583.
                                                                                                                                                                                                                                    Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1305;
                                                                                                                                                                                                                                                                                                        151 DYDA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                              1 DYDA 4
                                                                                                                                                                                                                                                                                                                                                                          TPX_STRSA P31308;
                                                                                                                                                                            INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INIT_MET SEQUENCE
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                               TPX_STRSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "TWO globin strains in the giant annelid extracellular haemoglobins.";
Blochem. J. 241:441-445(1987).
-!- SUBUNIT: THE EXTRACELULAR HEMOGLOBIN OF THE EARTHWORM CONSISTS
OF 12 SUBUNITS THAT HAVE A HEXAGONAL BILAYER STRUCTURE WITH A MOLECULAR WEIGHT NEAR 3.8 MILLION. EACH ONE-TWELFTH SUBUNIT IS COMPOSED PRIMARILY OF DISULFIDE LINKED TRIMERS (CHAINS A, B,
                                                                                                              Jahlang S.M., Riggs A.F.;
"The structure of the gene encoding chain c of the hemoglobin of the earthworm, Lumbricus terrestriss.";
J. Blol. Chem. 264:19003-19008(1989).
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 18-170.
MEDLINE-88198209; PubMed-3360792;
Fushitani K., Matsuura M.S.A., Riggs A.F.;
"The amino acid sequences of chains a, b, and c that form the trimer subunit of the extracellular hemoglobin from Lumbricus terrestris.";
J. Blol. Chem. 263:6502-6517(1988).
Lumbricus terrestris (Common earthworm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87241210; PubMed-3593201;
Gotoh T., Shishikura F., Snow J.W., Ereifej K.I., Vinogradov S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                               Jhiang S.M., Garey J.R., Riggs A.F.; "Exon-intron organization in genes of earthworm and vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH CHAIN IV)
(BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLOBIN III, EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> T (IN REF. 2).
03306F66E8BE3057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; 1
Pred. No. 1.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND C) AND MONOMERS (CHAIN D). SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxygen transport; Transport; Signal.
                                Lumbricidae; Lumbricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, J03082; AAA75013.1; -.
EMBL, J05161; AAA98622.1; -.
PIR, A28563; A28563.
PIR, C28151; C28151.
PIR, A34433, A34433.
InterPro; IPR002336; Erythcrurin.
InterPro; IPR000371; G10bin.
                                                                               SEQUENCE FROM N.A.
MEDLINE-90037024; PubMed-2808405;
                                                                                                                                                                                                                 MEDLINE=88178114; PubMed=2832953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERYTHCRUORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 AA; 19082 MW;
                                                                                                                                                                                                                                                                                   Science 240:334-336(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01033; GLOBIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00042; globin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170
23
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Best Local Similarity
                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 18-39.
                                  Lumbricina; Lumb
NCBI_TaxID=6398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Walz D.A.;
                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                   globins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-RG / KN20 / ATCC 51907;

MEDLINE-95350630; Pubmed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Sortt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 11, Created)
(Rel. 13, Last sequence update)
(Rel. 41, Last annotation update)
extracellular precursor (Erythrocruorin) (Globin C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).
-!- FUNCTION: NOT KNOWN, LACK THE PHOSPHORYLATION SITE FOUND IN
OTHER PISN PROTEIN:
-!- SIMILARITY: BELONGS TO THE PIS IIA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuck; nill.
Interpro; IRR002178; PTS_EIIA_2.
Pfam; PF00359; PTS_EIIA_2; 1.
ProDom; PD001689; PTS_EIIA_2; 1.
PROSITE; PS00372; PTS_EIIA_2; FALSE_NEG.
Phosphotransferase system; Complete proteome.
SEQUENCE 164 AA; 18444 MW; A71EBDD5C2738611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; 1
llarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0;
                                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 AA
                                                                                                                164 AA
                                                                                                                                                                                                Nitrogen regulatory IIA protein homolog.
PTSN OR HI1147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32794; AAC22802.1; -. HSSP; P31222; 1A6J.
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                 Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
**Local 4; Conserve
                                                                                                                                                                                                                                                                                   NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGR; HI1147; -
                             DYDA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989
01-JAN-1990
15-JUN-2002
Globin III,
                                                                                                                                                   01-NOV-1995
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91 DYDA 94
1 DYDA 4
                                                                                                                                                                01-NOV-1995
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P11069;
                                                                                                                PTSN_HAEIN
P45072;
                                                                                          GLB3_LUMTE

1D GLB3_LU

AC P11069;

DT 01-JUL-

DT 15-JUN-

DE Globin
                               151
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Gaps

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Best Loca
Matches
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                                                                                                                                                                                                                                   STRAIN-Mu50 / ATCC 700699, and N315;
STRAIN-Mu50 / ATCC 700699, and N315;
STRAIN-Mu50 / ATCC 700699, and N315;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchl A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Nhole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22040717; Pubmed=12044378;
Baba T., Takeuchi F., Kuroda M., 'Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borchardt S.A., Babwah A.V., Jayaswal R.K.; "Sequence analysis of the region downstream from a peptidoglycan hydrolase-encoding gene from Staphylococcus aureus NCTC8325."; Gene 137:253-258(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
3632 MW; A571A08B0FD0D719 CRC64;
                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein SAV1875/SA1692/MW1815 (ORFI).
SAV1875 OR SA1692 OR MW1815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sene 13/:253-258(1993).
-1- SIMILARITY: BELONGS TO THE THIJ / PFPI FAMILY.
                                                                                                                                          Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315),
                                                                                                                                                                                  Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; L
Pred. No. 1.2e+02;
                                                171 AA.
                                                                                                                                                                     Staphylococcus aureus (strain MW2), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=NCTC 8325;
MEDLINE=94131293; PubMed=7905453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AP003363; BAB58037.1; -. EMBL, AP003135; BAB42961.1; -. EMBL, AP004828; BAB95680.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lancet 359:1819-1827(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002818; ThiJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L19300; AAA18514.1;
MEROPS; C56.UPW; -.
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                           YI75_STAAM
Q53719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MW2
                 RESULT 37
YI75_STAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                 Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHICH
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Bowman's gland;
MEDLINE=87149013; PubMed=3493528;
Lee K.-H., Wells R.G., Reed R.R.;
Lisolation of an olfactory cDNA: similarity to retinol-binding protein suggests a role in olfaction.";
Protein suggests a role in olfaction.";
Protein SPECIFICITY: SYNTHESIZED IN THE BOWMAN'S GLANDS, WHI SECRETE THE MUCUS THAT BATHES THE CILIA OF THE OLFACTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLFACTORY PROTEIN.
BY SIMILARITY.
61499AF22E72D251 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease inhibitor 2 (PSPI-21) (PSPI-21-5.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; 100.0%; Pred. No. 1.3e+02; 1ve 0; Mismatches 0;
                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                 177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A25837; OVFGP.
InterPro; IPR000566; Lipocln_cytFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00061; lipocalin; 1. PROSITE; PS00213; LIPOCALIN; 1. Olfaction; Signal; Lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last seq
01-0CT-1996 (Rel. 34, Last ann
01factory protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 AA; 20191 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M15531; AAA49529.1; -.
                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEUROEPITHELIUM
                                                                                                                                                                                                        01-JAN-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8404;
                          |||||
64 DYDA 67
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SPI2_SOLTU
ID SPI2_SOLTU
AC P58515;
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                                                                                                                                                               OLFA_RANPI
P06910;
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1 DYDA
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                                                                                                                                         OLFA_RANPI
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Gaps

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Indels

0; Mismatches

4; Conservative

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                                                                                                                                      B101. Chem. 381:1215-1221(2000).

-!- FUNCTION: POTEWI INHIBITOR OF SERINE PROTEASES (CHYMOTRYPSIN AND TRYPSIN. INHIBITS TIGHTLY HUMAN LEUKOCYTE ELASTASE (HLE). DOES NOT INHIBIT PAPAIN, PEPSIN NOR CATHEPSIN D (CYSTEINE AND ASPARTIC PROTEASES). PROTECTS THE PLANT BY INHIBITING PROTEASES OF INVADING ORGANISMS, DECREASING BOTH HYPHAL GROWTH AND ZOOSPORES GERMINATION OF PHYTOPHTHORA INFESTANCE.
- SUBUNIT: HETERODIMER OF CHAINS A AND B; DISULFIDE-LINKED. DOUBLE-HEADED INHIBITOR ABLE TO FORM TRIPLE COMPLEXES WITH TARGET PROTEASES, BY BINDING SIMULTANEOUSLY ONE MOLECULE OF TRYPSIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANCELLANGOUS: THE SERINE PROTEASE INHIBITOR PSPI-21 COMPRISES TWO PROTEIN SPECIES WITH PI 5.2 AND 6.3, DENOTED AS PSPI-21-5.2 AND PSPI-21-6.3. THEY MAY BE ENCODED BY TWO ALLELES AT THE SAME GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN B.

REACTIVE BOND (FOR TRYPSIN).

REACTIVE BOND (FOR CHYMOTRYPSIN OR HLE).

REACTIVE BOND (FOR CHYMOTRYPSIN OR HLE).

INTERCHAIN (BY SIMILARITY).

26C19E0BBBA01E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Vacuolar (By similarity).
-i- TISSUE SPECIFICITY: TUBERS.
-i- INDUCTION: By infection with Phytophthora infestans.
-i- PTM: PROBABLY SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR WHICH IS CLEAVED TO FORM CHAIN A AND CHAIN B.
-i- MASS SPECTROMETRY: MW=16396; MW_ERR=16; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASS SPECTROMETRY: MW-4182; MW_ERR-4; METHOD=Electrospray;
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                     MEDLINE-21077058; Pibmed-11209756;
Valueva T.A., Revina T.A., Mosolov V.V., Mentele R.;
"Primary structure of potato kunitz-type serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SCO7215 OR SC2H12.14C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD000891; Kunitz_legume; 1.
SM00452; STI; 1.
S; PS00283; SOYBEAN_KUNITZ; 1.
protease inhibitor; Multigene family.
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186
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116
97
Istrinski1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANGE=151-187
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09K470;
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                                                                                                                   inhibitor.
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PROSITE;
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NON_CONS
CHAIN
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DISULFID
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"Kunitz-type proteinase inhibitors from intact and
Phytophthora-infected potato tubers.";
FEBS Lett. 426:131-134(1998).

-!- FUNCTION: POTENT INHIBITOR OF SERINE PROTEASES (CHYMOTRYPSIN AND
TRYPSIN). INHIBITS TIGHTLY HUMAN LEUKOCYTE ELASTASE (HLE). DOES
NOT INHIBIT PAPAIN, PERSIN NOR CAHERSIN D (CYSTEINE AND ASPARTIC
PROTEASES). PROTECTS THE PLANT BY INHIBITING PROTEASES OF INVADING
ORGANISMS, DECREASING BOTH HYPHAL GROWTH AND ZOOSPORES GERMINATION
OF PHYTOPHTHORA INFESTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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SUBCELLULAR LOCATION: Vacuolar (By similarity).
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Nell S., Sabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-- SIMILARITY: BELONGS TO THE UPF0157 (GRPB) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Istrinskii;
MEDLINE=21077058; PubMed=11209756;
Valueva T.A., Revina T.A., Mosolov V.V., Mentele R.;
Primary structure of potato kunitz-type serine proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL359215; CAB94638.1; -. Hypothetical protein; Complete proteome. SEQUENCE 186 AA; 20757 MW; 38545B835F9C09DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease inhibitor 1 (PSPI-21) (PSPI-21-6.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=98258940; PubMed=9598993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 381:1215-1221(2000).
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Best Local Similarity Juv..
نام 4; Conservative
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                                                                                                                                                                                                                              Hopwood D.A.;
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30 DYDA 33
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P58514;
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RESULT 43
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                                                                             RANGE-151-187.
MISCELLANEOUS: THE SERINE PROTEASE INHIBITOR PSPI-21 COMPRISES TWO PROTEIN SPECIES WITH PI 5.2 AND 6.3, DENOTED AS PSPI-21-5.2 AND PSPI-21-6.3. THEY MAY BE ENCODED BY TWO ALLELES AT THE SAME GENE
                                                                                                                                                                                                                                CHAIN B. REAÇTIVE BOND (FOR TRYPSIN). REACTIVE BOND (FOR CHYMOTRYPSIN OR HLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang W., Ni L., Somerville R.L.; "A stationary-phase protein of Escherichia coli that affects the mode of association between the trp repressor protein and operator-bearing
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
           -!- INDUCTION: By infection with Phytophthora infestans.
-!- PTM: PROBABLY SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR WHICH IS CLEAVED TO FORM CHAIN A AND CHAIN B.
-!- MASS SPECTROMETRY: WW-16078; WM_ERR-16; METHOD-Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                               SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
                                                               MASS SPECTROMETRY: MW=4282; MW_ERR=4; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 187; 100.0%; Pred. No. 1.4e+02; Pred. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mau B., Shao Y.;
"The complete genome sequence of Bscherichia coll K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                         INTERCHAIN.
6AFE7F4AAAFD706B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        WRBA_ECOLI STANDARD; PRT; 197 AA. P30849; P75890; P77543; P01-JU-1993 (Rel. 26, Created) 1-JU-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Flavoprotein wrbA (Trp repressor binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 90:5796-5800(1993)
                                                                                                                                                  InterPro; IPR002160; Kunitz_legume.
ProDom; PD000891; Kunitz_legume; 1.
SMART; SM00452; STI, 1.
SMOSITE, PS00283; SOYBEAN KUNITZ; 1.
Serine protease inhibitor; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-18
                                                                                                                                                                                                           CHAIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93296226; PubMed=8516330;
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151
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MEDLINE-97061202; PubMed-8905232;
  SPECIFICITY: TUBERS
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                   115
48
146
187 AA;
                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                     RANGE=1-150
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                                                                                                                                            FAMILY.
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ACT_SITE
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                    SEQUENCE
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of multimeric flavodoxin-like proteins.";

1. Biol. Chem. 273:20960-20966(1998).

2. Biol. Chem. 273:20960-20966(1998).

2. FOUTION: Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. However, with does not specifically influence the affinity or mode of binding of trpR to its operator. It seems possible that the association may have a structural, rather than functional, basis. WrbA alone does not interact with the operator-bearing DNA; the trpR/trpO complex is probably the major target species. The wrbA protein may function as an accessory element in blocking trpR-specific transcriptional processes that might be physiologically disadvantageous in the stationary phase of the bacterial life cycle.

2. SUBUNIT: Homodimer and homotetramer; in equilibrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               founding member of a new family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                           STRAIN=JM101;
MEDLINE-98361966; PubMed-9694845;
Grandori R., Khalifah P., Boice J.A., Fairman R., Giovanielli K.,
                                                                                                                                                    Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
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7B48C7CC2B71747 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Flavoprotein wrbA (Trp repressor binding protein).
WRBA OR SYX1155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 AA.
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PROSITE; PS00201; FLAVODOXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-10, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Biochemical characterization of WrbA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavoprotein; FMN; Complete proteome.
INIT_MET 0 0 CONFLICT 141 141 G -> A (
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InterPro; IPR001226; Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE000202; AAC74089.1; -. EMBL, D90738; BAA35781.1; -. EMBL, D90737; BAA35771.1; -. SWISS-2DPAGE; P30849; COLI.
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67 DYDA 70
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Q827N9;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Carey J.;
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SPECIES=H.cutirubrum;
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                                                                                                                                                                     Parkhill J., Dougan G., James K. D., Thomson N.R., Pickard D., Wain J.,
A Barkill J., Dougan G., James K. D., Holden M.T.G., Sebaihia M.,
A Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
A Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
A Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
A Whitehead S., Barrell B.G.;
Micherded S., Barrell B.G.;
T. Complete genome sequence of a multiple drug resistant Salmonella enteriora serovar Typhi CT18.";
Dature 413:848-852(2001).
C. I- FUNCTION: Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA (By similarity).
C. I- SIMILARITY: BELONGS TO THE WRBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21534948; PubMed=11677609; MEDLINE-21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WRBA OR STW1119.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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DCD65E43E98C7112 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Flavoproteth wrbA (Trp repressor binding protein).
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Pfam; PF00258; flavodoxin; 1.
PROSITE; PS00201; FLAVODOXIN; FALSE_NEG.
Flavoprotein; FMN; Complete proteome.
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                                                                                                               SEQUENCE FROM N.A.
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  Salmonella typhi
                                                                  NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=602;
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67 DYDA 70
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15-JUN-2002 (
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WRBA_SALTY
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MINE-20504483; PubMed=11016950;
Shukia H.D., Lasky S.P., Mahairas G.G., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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SPECIES=H.cutirubrum;
MEDLIKE=8930846; PubMed=2745441;
MEDLIKE=89308646; P.P.;
"Evolution and regulation of the gene encoding superoxide dismutase from the archaebacterium Halobacterium cutirubrum.";
J. Biol. Chem. 264:12253-12258(1989).
                        noncovalent complexes between the trp repressor protein and operator-bearing DNA (By similarity).
-!- COFACTOR: BILG'S TO THE MOROMER (By similarity).
-!- SIMILARITY: BELONGS TO THE MENA FAMILY.
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Nature 413:852-856(2001).
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
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Halobacteriaceae; Halobacterium.
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INIT_MET 0 0 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00258; flavodoxin; 1.
PROSITE; PS00201; FLAVODOXIN; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG????; wrbA.; IPR001226; Flavodoxin.
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SEQUENCE FROM N.A.
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                                                                                                                                                                             SEQUENCE OF 1-56.

SPECIES-H.cutirubrum;

MEDLINE=7165744; Pubmed=3104309;

MAP B.P., Dennis P.P.;

"Superoxide dismutase from the extremely halophilic archaebacterium cutirubrum.";

"Bacteriol. 169:1417-1422(1887).

"I Bacteriol. 169:1417-1422(1887).

"I CAPALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

"COFFACTOR: Manganes."

"SUBONIT: HOMOCHECTAMER (Probable).

"SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
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                                May B.P., Tam P., Dennis P.P.; 'The expression of the superoxide dismutase gene in Halobacterium cutirubrum and Halobacterium volcanii."; Can. J. Microbiol. 35:171-175(1989).
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E -> N (IN REF. 4).
2D3CC5664F811719 CRC64;
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Pred. No. 1.5e+02;
0; Mismatches 0;
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MEDLINE=89248676; PubMed=2720491;
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22254 MW;
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Similarity 100.0%;
4; Conservative 0
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199 AA;
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Search completed: February 6, 2003, 11:16:42 Job time : 8.3333 secs

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082144 yersinia pe
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STRAIN-ATCC 2743(KID):
STRAIN-ATCC 275641; PubMed-7476192;
MEDLINE-96059641; PubMed-7476192;
BOTK P., Ouzounis C., Casari G., Schneider R., Sander C., Dolan M., Gilbert W., Gillevet P.M.;
Gilbert W., Gillevet P.M.;
Exphoring the Mycoplasma capricolum genome: a minimal cell reveals its physiology.
Mol. Microbiol. 16:955-967(1995).
EMBL: 333203; CARB3788.1; -.
InterPro; IPRO01437; GreA_GreB.
Probom; PRO0449; GreA_GreB.
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                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Entomoplasmatales; Entomoplasmataceae.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q81229
Q9A859
Q9HNJ7
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Mycoplasma capricolum.
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SEQUENCE 42 AA;
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049040;
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O8zxz7 pyrobaculum
O17545 caenorhabdi
Q94194 atropa bell
Q8tv22 methanopyru
Q92jx2 rhizobium m
Q8u9h5 agrobacteri
Q8ujm5 agrobacteri
Q8vjf8 mycobacteri
Q8vjf8 mycobacteri
Q8vjf9 homo sapien
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Copyright (c) 1993 - 2003 Compugen Ltd.
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53 DYDA 56
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                  Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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Pred. No. 1.9e+02;
Mismatches 0; Indels
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EMBL; AJ002906; CAA05741.1; .
InterPro: IPR000719; Buk pkinase.
Pfam: PROACG: nkinase.
                                                                                                                                                          Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
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5781 MW; ACC8 07B59F33AB31 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Protein tyrosine kinase (EC 2.7.1:112) (Fragment).
CEHD-28.
                                                                                                    Last annotation update)
                                                                                    Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99;984-989(2002).
EMBL; AE009799; AAL63199.1; -.
Complete proteome.
SEQUENCE 45 AA; 4568 MW. RRPOGENTALINE.
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Oates A.C., Wilks A.F.;

"How many PTKs to organise a worm?";

The Worm Breeders Gazette 14:87-87(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                               Created)
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-IM2 / ATCC 51768 / DSM 7523; PubMed-11792869;
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                                                           01-MAR-2002 (TIEMBLRE1. 20, CIE
01-MAR-2002 (TIEMBLRE1. 20, Las
01-MAR-2002 (TIEMBLRE1. 20, Las
Conserved within P. aerophilum.
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                                                                                                                                                                                                     Thermoproteaceae; Pyrobaculum
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Kinase; Transferase.
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Best Local Similarity
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                                                                                                                                                                                                                     NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                      Miller J.H.;
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RESULT
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                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTW-2002 (TrEMBLrel. 21, Last annotation update)
01-DTW-2002 (TrEMBLrel. 21, Last annotation update)
Dutative ribosomal-like protein (Fragment).
Atropa belladonna (Belladonna) (Deadly nightshade):
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Asteridae; euasterids; sudicotyledons; core eudicots;
NCBI_TaxID=33113;
                                                                                                                                                                                                                                                                                                    Nouar E., Baucher M., Jaziri M.; "Differential gene expression in Atropa belladonna leafy gall."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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; Pred. No. 2.5e+02;
0; Mismatches 0;
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Pred. No. 2.8e+02;
Mismatches 0;
    58 AA.
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STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; Pubmed=11930014;
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01-Jun-2002 (TrEMBLrel. 21, La
01-Jun-2002 (TrEMBLrel. 21, La
Ferredoxin.
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EMBL; AE010447; AAM02792.1;
Complete proteome.
SEQUENCE 63 AA; 6690 MW;
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Best Local Similarity 100...
4; Conservative
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PRELIMINARY;
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MEDLINE-21608551; PubMed-11743194;
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Best Local Similarity
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Q8UJM5
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                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-2136507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizoblum meliloti strain 1021 ";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                    Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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SEQUENCE 67 AA; 7733 MW; 94416A9E2191AF32 CRC64;
                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein R02784.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
4 Hypotherical protein Atu3753.
ATU3753 OR AGR.L. 2160.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                               PRELIMINARY;
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                7 DYDA 10
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22 DYDA 25
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L., Durollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Moullam C., Cardon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Gurson J., Lomo C., Sear C., Strub G., Greone sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CSB."; EMBL, AE009306; AL44563.1; BMBL, AE009306; AL44563.1; BMBL, AE009306; AL44563.1; Hypothetical protein; Complete proteome.
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MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Cao Y., Askenazi M., Halling C., Mullin L.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
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"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tunefactens C58.";
Science 294.2333-2328(2001).
EMBL; AE008965; AAL46138.1; -.
EMBL; AE007913; AAK90826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 16; Length 67; 100.0%; Pred. No. 38+02; ive 0; Mismatches 0; Indels
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SEQUENCE 68 AA; 7596 MW; E42F36903AA88FB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu5451.
Agr05451 OR AGR PAT_662.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
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100.0%;
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NCBI_TaxID=176299;
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SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                                  NCBI_TaxID=4081;
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DYDA 60
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68 DYDA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-JRS4;
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    DYDA
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SEQUENCE
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NON_CONS
NON_TER
SEQUENCE
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NON_CONS
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P82571;
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P82571
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINS-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                               Bacteria; Firmicutes; Actinobactéria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB00/097; AAK46939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 16; Length 69;
Pred. No. 3.1e+02;
0; Mismatches 0; Indels
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC00/789; AAH07583.1;
InterPro: IPR001014; Ribosomal_L23;
Pfam; PF00276; Ribosomal_L23; 1.
ProDom; PD001141; Ribosomal_L23; 1.
PROSITE; PS000141; Ribosomal_L23; 1.
PROSITE; PS000161; Ribosomal_L23; UNKNOWN 1.
SEQUENCE 70 AA; 7923 MW; AC1C466548F343C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                    al protein.
69 AA; 7386 MW; 2F23B964568A2046 CRC64;
                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MYPOtherical protein MT2627.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
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0
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Unknown (protein for MGC:15572).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 4; L
100.0%; Pred. No. 3.1e+02;
Live 0; Mismatches 0;
                                                                                              69 AA
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  Mismatches
                                                                                              PRT;
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0
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100.0%;
                                                                                                                                                                     Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 4; Conservative
 Conservative
                                                                                              PRELIMINARY;
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Best Local Similarity
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TISSUE=PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                  DYDA 36
                                                                                                                                                                                                                                                                                                                                                     Hypothetical
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43 DYDA 46
                     1 DYDA 4
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 4
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                                                                                            Q8VJF8
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                                         33
Matches
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                                                                                  Q8VJF8
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Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J., VanBogelen R.A.; "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypoxia-induced hypothetical protein 162 (Fragment).
Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. ALLSA CRAIG;
Aggelis A.K.,
Aggelis A.K.,
"Hypoxia-induced cDNAs isolated by RNA differential display.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF081024; AAD46143.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins.";
Submitted (MAY-2000) to the SWISS-PROT data bank.
-!- MASS SPECTROMETRY: MW-49603.57; METHOD-ELECTROSPRAY.
InterPro; IPR001137; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2C1B214D33B2184E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 10;
100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
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Pred. No. 3.6e+02;
  72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLRel. 15, Created)
01-OCT-2000 (TrEMBLRel. 15, Last sequence
01-JUN-2001 (TrEMBLRel. 17, Last annotation of the protein from 2D-page (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
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Les 4; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
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86 AA.

Created)

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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-93127147; PubMed-1481201; Zemmour J., Parham P.; TA ribosomal protein-like sequence in the 3' untranslated region of the HLA-F gene.";
                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 86 AA; 10155 MW; 004390A546FDA93A CRC64;
                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ribosomal-like PROTEIN-HLA-F product (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical CF-8 family protein CAC0553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodom; PD001141; Ribosomal_L23; 1.
PROSITE; PS00050; RIBOSOMAL_L23; UNKNOWN_1
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; Pubmed-11465286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Antigens 40:250-253(1992).
InterPro; IPR01014; Ribosomal_L23.
Pfam; PF00276; Ribosomal_L23; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA; 9565 MW;
                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium acetobutylicum.
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Matches 4; Conservative
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                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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73 DYDA 76
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SEQUENCE
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                                                                                          Q9TNR9
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Q97LK6
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Breiman R.F., Gratten M., Hollingshead S.K., Briles D.E., Crain M.J.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AR036621, ARC09243.1;
EMBL, AF036622, ARC09240.1;
EMBL, AF036622, ARC09240.1;
EMBL, AF036622, ARC09241.1;
EMBL, AF036622, ARC09242.1;
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Breiman R.F., Gratten M., Hollingshead S.K., Briles D.E., Crain M.J.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF036620; AAC09239.1; -.
ROBL, AF036619; AAC09238.1; -.
NON_TER 85
SEQUENCE 85 AA; 9327 MW; CF4C467ACAB4868E CRC64;
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA; 8879 MW; 3752E31D97028C0A CRC64;
                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
PNEUMOCOCCAL surface protein A (Fragment).
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Last annotation update)
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  Mismatches
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01-AUG-1998 (TrEMBLrel. 07, Last sequence
01-AUG-1998 (TrEMBLrel. 07, Last annotation
PMEUMOCOCCAL surface protein A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae.
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les 4; Conservative
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  Conservative
                                                                                                                                                                                                       PRELIMINARY;
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tes 4; Conserv
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45 DYDA 48
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45 DYDA 48
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  4;
                                          1 DYDA 4
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Gaps

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Length 86; Indels

100.0%; Score 23; DB 7; 1 100.0%; Pred. No. 3.9e+02;

0; Mismatches

86 AA.

PRT;

05ED08ED596CD6EE CRC64;

Gaps

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100.0%; Score 23; DB 16; Length 86; 100.0%; Pred. No. 3.9e+02; Live 0; Mismatches 0; Indels

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ProDom; PD000544; PV_capsid_L1; 1.

NON_TER 1 1

NON_TER 92 92

SEQUENCE 92 AA; 10490 MW: 9675
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072138;
01-8UG-1998 (TEMBLEEL 07,
01-8UG-1998 (TEMBLEEL 07,
01-DEC-2001 (TEMBLEEL 19,
                                                                                                                                                                         4; Conservative
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Matches 4; Conserv
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NCBI_TaxID=10566;
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|15 DYDA 18
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MEDLINE-20295075; PubMed=10834958;

MEDLINE-20295075; PubMed=10834958;

MEDLINE-20295075; PubMed=10834958;

MEDLINE-20295075; PubMed=10834958;

Persistence of Human Papillomavirus DNA in Benign and (Pre)malignant Skin Lesions from Renal Transplant Recipients.";

J. Clin. Microbiol. 3812087-2096(2000).

EMBL: AF054879; AAC12745.1;

InterPro; IPR002210; PV_capsid_L1.

Pfam; PF00500; late_protein_L1; 1.
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
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InterPro; IPR005290; RS15_bact.
Pfam: PF00312; Ribosomal_S15; 1.
IIGRFAMS; IIGR00952; S15_bact. 1.
PROSTIE; PS00322; RIBOSOMAL_S15; 1.
Ribosomal protein; Complete protecome.
SEQUENCE 91 AA; 10151 MW; AC8601PDF567D2BF CRC64;
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(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                               Last sequence update)
Last annotation update)
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EMBL; AE001894; AAF09921.1; -.
HSSP; P80378; 1AB3.
                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                  Deinococcaceae; Deinococcus
                                                                                                                       PRELIMINARY;
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Human papillomavirus.
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NCBI_TaxID=10566;
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01-AUG-1998 (
01-DEC-2001 (
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"Persistence of Human Papillomavirus DNA in Benign and (Pre)malignant Skin Lesions from Renal Transplant Recipients.";
J. Clin. Microbiol. 38:2087-2096(2000).
EMBL; AF054880; AAC12746.1;
-InterPro: IPR002210; PV_capsid_L1.
Probom; PD0000544; PV_capsid_L1; 1.
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                                              Length 92;
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Papillomavirus.
NCBI_TaxID=10566;
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
9675649BBB8C4901 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
                                          Score 23; DB 12;
Pred. No. 4.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                92 AA.
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072134;
01-3UG-1998 (TrEMBLrel. 07, Created)
01-MG-1998 (TrEMBLrel. 07, Last sequer
01-DEC-2001 (TrEMBLrel. 19, Last annote
LI protein (Fragment)
Human papillomavirus.
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MEDLINE=20295075; Pubmed=10834958;
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MEDLINE=20295075; PubMed=10834958;
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100.0%;
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MEDLINE-21074935; PubMed-11206551;
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Persistence of Human Papillomavirus DNA in Benign and (Pre)malignant Skin Lesions from Renal Transplant Recipients.";
J. Clin. Microbiol. 38:2087-2096(2000).
EMBL; AF054887; AAC12753.1;
Interpro; IPR002210; PV_capsid_L1.
Pfam; PF00500; late_proctein_L1; 1.
Probom: PD000544; PV_capsid_L1; 1.
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Escherichia.
          Mulder L.H.C., Berkhout R.J.M., Boxman I.L.A., ter Schegget J.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054884; AAC12750.1; -.
Interpro; IPR002210; PV_capsid_L1.
ProDom; PF00500; late_protein_L1; 1.
NON_TER 1 1 1.
NON_TER 1 2 2.
SEQUENCE 92 AA; 10613 MW; A6F64813AFE90474 CRC64;
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Pred. No. 4.2e+02;
Mismatches 0; Indels
                                                                                                                                                                                                            Length 92;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
19501betical protein 20510.
19501 OR ECS0462.
Escherichia coli 0157:H7.
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Last annotation update)
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100.0%; Pred. No. 4.2e+02;
iive 0; Mismatches 0;
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
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MEDLINE-20295075; PubMed-10834958;
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100.0%;
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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NCBI_TaxID=10566;
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STRAIN-HPVX27;
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15 DYDA 18
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SEQUENCE
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072141;
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Q8XE95;
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Matches
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12."; EMBL; AE005220; AAG54758.1; -.
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MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Genome sequence of Persinia pestis, the causative agent of plague.";
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Aroback E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
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EMBL: AJ414142; CAC89252.1; --
Hypothetical protein: Complete proteome.
SEQUENCE 95 AA: 10766 WW: 234C33AD38A547CC CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein YPO0394.
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100.0%; Pred. No. 4.3e+02;
ative 0; Mismatches 0;
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100.0%; Pred. No. 4.4e+02;
iive 0; Mismatches 0;
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MEDLINE-21156231; PubMed-11258796;
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                      Whole genome
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4 DYDA 7
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XX MEDLINE-98295987; PubMed-9634230;

XA COLG S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Cordon S.V. Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Bales R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RR Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RR Complete genome sequence.";

RL Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRANN-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Peterson J., DeeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                     suppression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
60S ribosomal protein (Fragment).
0ncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
0ncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                               Bayne C.J., Gerwick L., Fujiki K., Nakao M., Yano T.;
"Immune-relevant (including acute phase) genes identified in the livers of rainbow trout, Oncorhynchus mykiss, by means of suppressubtractive hybridization.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ARS1349, AAG30009.1;
InterPro: IPRO10104; Ribosomal_L23.
ProDom; PD001141; Ribosomal_L23: 1.
PROSITE; PS00050; RIBOSOMAL_L23; 1.
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                              96 AA.
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                             PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
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RESULT 24
Q9DFF6
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
comparison of Mycobacterium tuberculosis clinical and
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                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 296072; CAB0948911; -..
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                           TIGR; MT2773; -.
TubercuList; Rv2699c; -.
Hypothetical protein; Complete proteome.
SEQUENCE 100 AA; 10916 MW; 2C9FB2212A4C1334 CRC64;
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SEQUENCE 100 AA; 10969 MW; EFIAC8895604DAC6 CRC64;
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Last annotation update)
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100.0%; Pred. No. 4.6e+02;
M.comatches 0;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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100.0%; Pred. No. 4.6e+02;
ive 0; Mismatches 0;
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Nature 409:1007-1011(2001).
EMBL; U15181; AAA62937.1;
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno'
01764J (Hypothetical protein ML1026).
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Best Local Similarity
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Ghim S. Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
"Sequence analysis of the 30 kb region (182') of the Bacillus subtilis schromosome containing the cge cluster.";
Submitted (JUN-199') to the EMBL/GenBank/DDBJ databases.
EMBL, AF006665; AAB81163.1;
SEQUENCE 104 AA; 12083 MW; 59293981BC04543A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=20383900; PubMed=10930075;
Ozawa Y., Courvalin P., Galimand M.;
Otawa Y., Courvalin P., Galimand M.;
Identification of enterococci at the species level by sequencing of the genes for D-alanine: D-alanine ligases.";
Syst. Appl. Microbiol. 23:230-237(2000).
Syst. Appl. Microbiol. 23:230-237(2000).
HSSP; P07862; 110V.
InterPro; IPR000291; Dala_Dala_ligase.
Pfam; PF01820; Dala_Dala_ligas; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Enterococcaceae; Enterococcus.
                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                       Last sequence update)
Last annotation update)
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62 DYDA 65
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034372
ID 034372
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     RESULT 29
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                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98343808; PubMed-9680214;
Neely M.N., Frledman D.I.;
"Functional and genetic analysis of regulatory regions of coliphage
198: location of Shiga-like toxin and lysis genes suggest a role for
phage functions in toxin release.";
Mol. Microbiol. 28:1255-1267(1998).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 5; Length 102; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neely M.N., Friedman D.I.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034975; AAD04642.1; -
SEQUENCE 103 AA; 11901 MW; 9A76B21E0BACD0E5 CRC64;
                                                                                                                                                                       Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(198).
EMBL: 270757; CAA94799.1; --
SEQUENCE 102 AA: 11388 MW; 76CBD7C84E6BA695 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE-99077833; Pubmed-9858702;
Neely M.v. Friedman D.I.;
Agrangement and functional identification of region of lambdoid phage H-19B, a carrier of a Gene 223:105-113(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AA.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19, Protein 9p17.
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Les 4; Conservative
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                   2K287.3 protein.
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52 DYDA 55
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35 DYDA 38
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KADLINE-98044033; PubMed-9384377;

KADLINE-98044033; PubMed-9384377;

KADLINE-98044033; PubMed-9384377;

KADLINE-98044033; PubMed-9384377;

KADLINE-98044033; PubMed-9384377;

RA AZEVEDO V., Bertero M.G., Bessieres P., Bolottin A., Borohert S., Azevedo V., Bertero N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Dusterhoft A., Ebrilich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujlta M., Fujlta Y., Fumma S., Gallzzi A., Galleron N.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Lacinchard M., Nichin C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krooh S., Kumano M.,

Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

Raiger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

Satto T., Scanlan E., Schleich S., Schroeter R., Scotfone F.,

Takeuchi M., Tamakoshi A., Tanaka T., Tarkanshi H., Takematu K.,

Takeuchi M., Tamakoshi A., Yanamoto H., Vaniet F., Vassanotti A.,

Winters P., Wapa A., Yanameten E., Yoshikawa H., Danchin A.,

Winters P., Wapa A., Yanameten E., Yoshikawa H., Danchin A.,

Ray Parana A., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

Ray Parana A., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

Ray Parana A., Yanaka A., Yanaka B., Yanaka 
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                                                                                             Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 16; Length 105;
Pred. No. 4.9e+02;
0; Mismatches 0; Indels (
                                                                                                                                                                                             Wambutt R., Wedler H., Lapidus A., Sorokin A., Ehrlich D.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF015775; AAB12066.1;
EMBL; 299114; CAB13855.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 AA; 12186 MW; 03BCCA4E80E57663 CRC64;
034372;
01-378-1998 (TrEMBLrel. 05, Created)
01-378-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Best Local Similarity
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                                                                                                                                              NCBI_TaxID=1423;
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Q8Y188
ID Q8Y18
AC Q8Y18
DT 01-MA
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SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; Rapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharypa A., Lykidis A., Raznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Salkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
Proc. Natl. Acad Sci. U.S. 99:443-448(2002).
EMBL; AE009497; AALSI738.1;
EMBL; Commilete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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Finkelstein D.B., Drew M.C., Wing R.A., Mullet J.E., Jordan W.R.,
                                                                                                       Brucella melitensis.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF061508; AAC24573.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 107 AA; 11803 MW; 95B1E9462A1EBA03 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ribosomal protein L25 (Fragment).
01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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100.0%; Pred. No. 5.1e+02;
tive 0; Mismatches 0;
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                                                   Hypothetical protein BMEI0557.
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                                                                                                                                                        Brucellaceae; Brucella.
NCBI_TaxID=29459;
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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96 DYDA 99
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Pred. No. 5.1e+02;

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Best Local Similarity 100.
Matches 4; Conservative
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22 DYDA 25
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31 DYDA 34
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18 DYDA 21
                                           1 DYDA 4
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Q9BIF5
Q9BIF5
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Q8V6T9
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                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=ATCC 19089 / CB15;

STRAIN=ATCC 19089 / CB15;

STRAIN=ATCC 19089 / CB15;

MEDLINB-21173698; bubmed=11259647;

Nichman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20504483; PubMed=11016950; Meditae B., Pan M., Meditae S.B., Mahairas G.G., Thorsson V., Sbrogna J., Shuklan H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weil D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Genome sequence of Hallobaccerium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                   Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 109;
                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF01022: HTH_5; 1.

PRINTS; PR00778; HTHARSR.

SMART; SM00418; HTH_ARSR; 1.

DNA-binding; Transcription regulation; Complete proteome.

SEQUENCE 109 AA; 11029 MW; 9490CFF4AE0A4BC5 CRC64;
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SEQUENCE 109 AA; 12102 MW; 27C5648027548E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacterium sp. (strain NRC-1).
Archaea: Euryarchaeota; Halobacteria; Halobacteriaceae; Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
01.JUN-2001 (TrEMBLrel. 17, Created)
01.JUN-2001 (TrEMBLrel. 17, Last sequence update)
01.MAR-2002 (TrEMBLrel. 20, Last annotation update)
Transcriptional regulator, ArsR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 16; Best Local Similarity 100.0%; Pred. No. 5.1e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA
                                                                                                                                                                                                                                                                                                                                REGULATORS.
EMBL; AE005825; AAK23484.1; -.
TIGR; CC1505; -.
                                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR001845; HTH_ArsR.
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                                                                    Caulobacter crescentus
                                                                                                            NCBI_TaxID=155892;
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68 DYDA 71
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                                                                                                 Caulobacter
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                                                                                                                                                                                                                                                                                                   M.L.;
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                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=33771;
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Jacquin-Joly E., Francois M.-C., Nagnan-Le Meillour P.;
"Molecular cloning of a SAP homolog in Mamestra brassicae male
antennae.";
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SEQUENCE FROM N.A.
Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyall-Smith Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyall-Smith Sequence and transcription of halovirus HF2.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF222060; AAL54940.1;
Hypothetical protein.
SEQUENCE 110 AA; 12585 MW; 8B24D378DD0A6BCB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Sensory appendage protein-like protein.
                                                                      01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical 12.6 kDa protein.
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100.0%; Pred. No. 5.1e+02;
ive 0; Mismatches 0;
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                                                     01-MAR-2002 (TrEMBLrel. 20,
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Matches 4; Conservative
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AC 080205;
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100.0%; Score 23; DB 17; Length 109;

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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                        Methanobacterium phage psiM2.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=77048;
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Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 112;
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Pfister P., Wasserfallen A., Stettler R., Leisinger T.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

BMBL, AF065411; AAC27054.1; - |
Hypothetical protein. 330A9F4604303994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                             MEDLINE=99009353; PubMed=9791169;
Pfister P., Wasserfallen A., Stettler R., Leisinger T.;
"Molecular analysis of Methanobacterium phage psiM2.";
Mol. Microbiol. 30:233-244(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA; 11815 MW; 133E6D08B4702F5F CRC64;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last manotation update)
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Nature 409:1007-1011(2001).
EMBL; AL583925; CAC31790.1;
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MEDLINE=21128732; PubMed=11234002;
                                                                    Hypothetical 13.0 kDa protein.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative secreted protein.
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Best Local Similarity
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65 DYDA 68
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RESULT 40

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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole genome comparison of Mycobacterium tuberculosis clinical and
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 295558; CAB08970.1; -.
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Hypothetical protein; Complete proteome.
SEQUENCE 112 AA; 12117 MW; 8A3AF97188684AD4 CRC64;
                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv0559c.
RV0559C OR MTCY25D10.38C OR MT0585.
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01-MAR-2010 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 13.1 kDa protein.
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100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0;
    112 AA
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    PRT;
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EMBL; AE006956; AAK44808.1; -.
                                                                                   (TrEMBLrel. 04, (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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PRELIMINARY;
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SEQUENCE FROM N.A.
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95 DYDA 98
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         [1]
SEQUENCE 1
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SEQUENCE
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08VHK4
AC 08VHK,
DT 01-MA,
DT 01-MA,
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DT 01-JU,
DE Aggrei
OS Mus m
OC Bukar
OC Bukar
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                           Luo Y., Pfister P., Leisinger T., Wasserfallen A.; The Genome of Archaeal Prophage PsiM.00 Encodes the Lytic Enzyme Responsible for Autolysis of Methanothermobacter wolfeii."; J. Bacteriol. 183:5788-5792(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-21154917; PubMed-11230166;
MICHARDAN S., Well B., Wellenreuther R., Gassenhuber J., Glassl S. Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;
"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
Genome Res. 11:422-435(2001):
EMBL; AL136718; CAB66652.1;
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Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                Length 113;
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Pred. No. 5.3e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR301375; ARG3963.1; -.
Hypothetical protein:
SEQUENCE 113 AA; 13102 MW; EF48F6AAFD6C79D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 114 AA; 12801 MW; 2D88B8AA3551AA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 12.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CC0421.
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MEDLINE-21429258; PubMed-11544247;
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Best Local Similarity
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SEQUENCE FROM N.A.
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|DYDA 68
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|DYDA 81
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094008
10 096000
AC 094000
DT 01-MA
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SEQUENCE FROM N.A.
STRAINA-TUCC 19989 / CB15;
MEDLINE-21173698, PubMed-11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (Tregment).
Mus musculus (Mouse).
Mus mecazoa: (Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finan T.M., Aneja P., Chain P., Napper K., Golding B.;
"Mineral Phosphate Solubilization in Sinorhizobium meliloti.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY013584; AAG42546.1;
InterPro; IPR002818; ThiJ.
InterPro; IPR002818; ThiJ.
NON_TER 117 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114;
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114 AA; 12824 MW; 268FD7B404E4E50D CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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11arity 100.0%; Pred. No. 5.3e+02;
Conservative 0; Mismatches 0;
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RN [1]
RP SEQUENCE FROM N.A.
RA Daikou S., Glaeser K.E., Horner M., Davies E.M., Jeffcott L.B.;
RT "Expression of murine aggreenases.";
RI Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
BME InterPro. IRNO1590; Reprolysin.
BR PROSTTE; PS50215; ADAM_MEPRO; 1.
FT NON_TER 11 11
FT NON_TER 11 11
SQ SEQUENCE 117 AA; 12775 MW; 941853E69F4526C3 CRC64;
Autches 117 AA; 12775 MW; 941853E69F4526C3 CRC64;

QUETY MATCh
Best Local Similarity 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYDA 4
Db 78 DYDA 81

Search completed: February 6, 2003, 11:21:52
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Fragment of T.serg N. meningitidis 60 N. meningitidis 60 Cytokine-11ke pept Peptide #11929 enc Protein #9269 enco

T-cell epitope con E6 binding domain Integrin alpha-Vbe Fragment of T.serg

Run on:

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AAB46891
AAB46892
AAG86361
AAG87624
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AAB46867
AAB46870
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AAR97408
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AAY50486
AAY39913
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2003, 11:16:00; Search time 27.8333 Seconds (without alignments) 19.150 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
1	20	100.0	8	17	AAR97402	Streptococcal M p
7	20	100.0	80	17	AAR97403	Streptococcal M p
m	20	100.0	œ	22	AAB46882	Integrin alpha-Vb
4	20	100.0	80	22	AAB46539	Integrin alphav-b
S	20	100.0	8	22	AAB46581	Integrin alphaV-b
9	20	100.0	6	17	AAW01152	MAb 1.4 heavy cha
7	20	100.0	6	19	AAW44175	Monoclonal antibo
89	20	100.0	6	22	AAB46868	Integrin alpha-Vb
σ	20	100.0	6	22	AAB46869	Integrin alpha-Vb
10	20	100.0	6	22	AAB46871	Integrin alpha-Vb

	ALIGNMENTS	
RESU AAR9 ID	RESULT 1 AAR97402 ID AAR97402 standard; peptide; 8 AA.	
A.	AAR97402;	
X E	02-DEC-1996 (first entry)	
XX DE	Streptococcal M protein peptide, p145, fragment 145.1.	~
KW KW	Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;	
XXX	<pre>detection; mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy; diagnosis.</pre>	
yy SO	Streptococcus spp.	
Y Z S	WO9611944-A1.	
2 2 3	25-APR-1996.	
PF	16-OCT-1995; 95WO-AU00681.	
X	14-OCT-1994; 94AU-0008851.	
PA PA PA		
PA PA PA	(CSLC-) CSL LTD. (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. (UYME) UNIV MELBOURNE.	
XX PI	Cooper Ja, Good MF, Relf WA, Saul AJ;	-

Thu Feb

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Example 1; Page 10; 20pp; German.
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                                                                                                                                                                                                                                                                immunologically active conformation.

The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against pp. A Streptococci. Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used diagnostically to detect Ab.
                                                                                                                                              The present peptide is a fragment of the Streptococcal M protein peptide p145 (Pruksakorn et al. J. Immunol. 149: 2729-2735 (1992)), used in the construction of a novel chimaeric peptide (CP). The CP comprises a B-cell conformational epitope from within p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an
                                       New chimaeric peptide(s) including a conformational epitope -
inserted into a peptide having similar native conformation, useful
in vaccines and for determn. of minimal epitope(s) or for mapping
amphipathic helices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper; detection; mapping; opsonic antibody; vaccine; group A Streptococci; lamunotherapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimaeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful
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ilarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
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                                                                                                                      Example 13; Page 37; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR97403 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOT-) BIOTECH AUSTRALIA PTY LTD
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Matches 4; Conserv
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4 DLDA 7
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Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic; cytostatic; osteopathic; antiinflammatory; antibacterial; antipporlatic; vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic; ophthalmological; antiarthritic; antidicer; vasotropic; neuroprotective; alpha vbeta, 6-integrin receptor; thrombosis; tumor; cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis; osteoporosis; inflammation; infection; psoriasis; wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                            The present peptide is a fragment of the Streptococcal M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)), used in the construction of a novel chimaeric peptide (CP). The CP comprises B-cell conformational epitope from within p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GOW4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation.

The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies the CP can be used for immunotherapy and diagnosis, while the CP
in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be used diagnostically to detect Ab
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5
                                                                                         Example 13; Page 37; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB46882 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE19933173-A1
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DLDA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB46882;
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New octapepide compounds as alpha v beta 6 integrin inhibitors useful for treating and diagnosing heart disease, tumors, osteoporosis, fibrosis, inflammation, infection and psoriasis

Jonczyk A, Diefenbach B, Groth U, Zischinsky G;

WPI; 2001-113366/13.

(MERE) MERCK PATENT GMBH.

99DE-1029410. 99DE-1029410

26-JUN-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin; inhibitor; thrombolytic; cardiant; antiarteriosclerotic; cytostatic; osteopathic; antiinflammatory; antimicrobial; antipsoriatic; vulnerary; antiulcer; cerebroprotective; antianginal; antidiabetic; ophthalmological; anticheumatic; antiarthritic; vasotropic; nephrotropic; neuroprotective; thrombosis; coronary infarction; coronary heart disease; arteriosclerosis; tumor; osteoporosis; fibrosis; inflammation; infection; psoriasis; wound healing; gastrointestinal disorder; epithelial system;
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                         Length 8;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Integrin alphaV-beta6 inhibitor peptide SEQ ID NO 12.
                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 22; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note- "N-1-Ac-Arg"
                                                                                                                                                                                                                                                                                                                                                             AAB46539 standard, peptide; 8 AA.
                                                                                                                                                                                                                                         receptor inhibiting activity.
                                                                                                                                                                                                                                                                                                                                                                                             10-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory disorder.
                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                         8 AA;
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DLDA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                           Seguence
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ID AAB4
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28-DEC-2000

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This invention describes novel octapepide compounds (I) which have thrombolytic, cardiant, antiarteriosclerotic, cytostatic, osteopathic, thrombolytic, cardiant, antiarteriosclerotic, cytostatic, osteopathic, cardialmanial, antidiabetic, vulnerary, antialicer, cardiant, antidiabetic, ophthalmological, antidiabetic, ophthalmological, cardirheumatic, antiarthritic, vasotropic, nephrotropic and encurportective. The compounds were tested for their ability to compete with fibronectin for binding to alpha_vbeta_6 integrin receptors in vitro. The compounds are useful as alpha_vbeta_6 integrin inhibitors for the treatment of thrombosis, coronary infarction, coronary heart disease, arteriosclerosis, tunors, osteoporosis, fibrosis, inflammation, infection and psoriasis, and for healing wounds. They can also be used to treat respiratory and gastrointestinal disorders (e.g. ulcerative colitis or crohn's disease), apoplexy, angina pectoris, diabetic retinopathy, myopia, macular degeneration, ocular histoplasmosis, rheumatoid arthritis, osteoarthritis, rubeotic glaucoma, post angioplastic restenosis, acute kidney failure and multiple sclerosis. The compounds are also useful in diagnosis for detection and localization of pathological conditions affecting the epithelial system. They can be conjugated with biotin, radiolabels, marker proteins or antibodies for this purpose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin; inhibitor; thrombolytic; cardiant; antiarteriosclerotic; cytostatic; osteopathic; antinflammatory; antimicrobial; antipsoriatic; vulnerary; antiulcer; cerebroprotective; antianginal; antidiabetic; ophthalmological; antirheumatic; antiarthritic; vasotropic; nephrotropic; neuroprotective; thrombosis; coronary infarction; coronary heart disease; arteriosclerosis; tumor; osteoporosis; fibrosis; inflammation; infection; psoriasis; wound healing; gastrointestinal disorder; epithelial system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 22;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin alphaV-beta6 inhibitor peptide #19.
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                                                                                                                                                                                                                                                                                         Example 1; Page 20; 33pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB46581 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha_vbeta_6 integrin receptor.
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Best Local Similarity luv...
Lnc 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA;
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Modifled-site
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WPI; 1996-333946/33.
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                      WO9620959-A1.
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                                                                                                27-DEC-1995;
                                                                                                                                      9-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-1996;
27-JUN-1996;
                                                                                                                                                                                                                  Kawauchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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    δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel octapepide compounds (I) which have thrombolytic, cardiant, antiarterlosciercic, cytostatic, osteopathic, cardiant, antiarterlosciercic, cytostatic, osteopathic, cartiniflammatory, antianginal, antidiabetic, ophthalmological, cerebroprotective, antianginal, antidiabetic, ophthalmological, antiarthritic, vasorropic, nephrotropic and cartinific antiarthritic, vasorropic, nephrotropic and cartinific antiarthritic, vasorropic, nephrotropic and cartinific compete with fibronectin for binding very tested for their ability to compete with fibronectin for binding to alpha_vbeta_6 integrin receptors in the reatment of thrombosis, coronary hadronic, concary infection the treatment of thrombosis, coronary inferction, coronary heart disease, arteriosclerosis, tumors, osteoporosis, fibrosis, inflammation, infection and psoriasis, and for healing wounds. They can also be used to treat cerpiratory and gastroinfestinal disorders (e.g. ulcerative colitis or Crohn's disease), apoplexy, angina pectoris, diabetic retinopathy, myopia, macular degeneration, ocular histoplasmosis, rheumatoid arthritis, osteoarthritis, rubeoic glaucoma, post angioplastic cestenosis, acute kidney failure and multiple sclerosis. The compounds are also useful in diagnosis for detection and localization of pathological conditions affecting the epithelial system. They can be conjugated with blotin, radiolabels, marker proteins or antibodies for this purpose. The compounds are specific and selective for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                New octapepide compounds as alpha v beta 6 integrin inhibitors useful for treating and diagnosing heart disease, tumors, osteoporosis, fibrosis, inflammation, infection and psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis; cerebral infarction; acute kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAb 1.4 heavy chain CDR (MAb binds type II phospholipase A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                        Groth U, Zischinsky G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%; Score 20; DB 22; Similarity 100.0%; Pred. No. 7.8e+05; 4; Conservative 0; Mismatches 0;
                                      /note= "C-terminal amide"
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/note= "Ac-Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 32; 33pp; German.
                                                                                                                                                        99DE-1029410.
                                                                                                                                                                                                                                                                        Jonczyk A, Diefenbach B,
                                                                                                                                                                                                                                  (MERE ) MERCK PATENT GMBH.
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                                                                                                                                                                                                                                                                                                            WPI; 2001-113366/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                    Modified-site
                                                                            DE19929410-A1
                                                                                                                                                        26-JUN-1999;
                                                                                                                                                                                            26-JUN-1999;
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DLDA 6
                                                                                                                28-DEC-2000
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AAW0115
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Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice.with recombinant human type II phospholipase A2. Splean calls from the mice were tueed with mouse myeloma P3UI (P3x63x98.UI) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity.

Active clones were isolated including 12H5, 1.4 and 10.1. These supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly suitable for preclinical testing. This peptide sequence corresponds to the third complementary determining region of the heavy chain of the monoclonal antibody isolated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin; amelioration; kidney disorder; nephrotoxicity; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                        Yasunada T;
                                                                                                                                                                                                                                    Takasaki J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW44175 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 42; 69pp; Japanese.
                                                                                                                                                        (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-JP02241.
95WO-JP02714
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96JP-0167286.
                                                                            94JP-0340006
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Best Local Similarity 100.
Matches 4; Conservative
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This invention describes novel cyclic peptides (1), containing 8 amino acid residues and optionally further alpha,omega-aminocarboxylic acid residues. Cyclic peptides of formula Cyclo.(Arg.x.1-Asp.x.1-X.2-x.3-x.4-x.2-x.3-x.4-x.1) (1) and their salts and solvates. X.1 = Ser, Gly or Thr: X.2 = Leu, Ile, Nle, val or Phe; X.3 = Asp, Glu, Lys or Phe; X.4 = Gly, Ala or Ser; X.5 = Leu, Ile, Nle, val or Phe; X.6 = Arg, Har or Cys; R.1 = one or more omega-aminocarboxylic acid residues are length of 50-2500 mum; or is absent; the amino acid residues are length of 50-2500 mum; or is absent; the amino acid residues are coptionally derivatized and include b-as well as L-forms (in the case of coptionally derivatized and include b-as well as L-forms (in the case of coptionally active aminoacids). The products of the invention have antithrombotic, carddant, antidiabetic, ophthalmological, cerebroprotective, antianginal, antidiabetic, ophthalmological, cerebroprotective, antianginal, antidiabetic, ophthalmological, cerebroprotective, antidiabetic, ophthalmological, cerebroprotective, antianginal, antidiabetic, ophthalmological, cerebroprotective, antidiabetic, ophthalmological, cerebroprotective, antidiabetic, ophthalmological, cerebroprotective, antidiabetic, ophthalmological function of alpha_vbeta_6-integrin receptors, especially thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, thrombosis, osteoproresis, fibrosis, inflammation, infection, psoriasis and wound healing deficiency. Other disclosed disorders to be treated include apoplexy, angine pectoris, ophthalmological diseases, arteriosis, included apoplexy, angine pectoris, ophthalmological diseases, acteriosis, cubector glaucoma), rheumatoid arthritis, osteoarthritis, crohn's disease, atherosclerosis, restenosis after angioplasty, acute renal failure, renal inflammation or multiple sclerosis. (I) may be used to prepare affinity chromatography columns for purifying integrin controlled. (I) are well the are well characted and have good alpha_order_fi
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                                                                                                                                                                                                                                                                                                                                                New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections
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100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                         Goodman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB46869 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 5; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           itself. (I) are well tolerate
receptor inhibiting activity.
                                99DE-1033173
                                                                                            99DE-1033173,
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                                                                                                                                                                                                                                                                                    WPI; 2001-192448/20.
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Les 4; Conserv
                             15-JUL-1999;
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3 DLDA 6
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                                                                                                                                                                                                                         Jonczyk A,
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a complementary determining region (CDR) from monoclonal antibody 1.4 heavy chain against type II phospholipase A2, from the present invention. The present invention of thospholipase A2, from the present invention of kidney disorders (such as acute renal fallure) associated with the administration of cispatath for the treatment of cancer. The method comprises treatment with a monoclonal antibody which inhibits the activity of type II phospholipase A2 (particularly of type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to release type II phospholipase A3, and has the ability to a cell method can be used for suppressing the nephrotoxicity which is a characteristic feature of cisplatin administration, and therefore allowing more efficient used for suppressing th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                 oration of kidney disorders caused by cisplatin administration treatment with an antibody inhibiting type II phospholipase A2
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                              Takasaki
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/note- "6-aminohexanic acid"
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                                                                                                                                                                                                                                                                                                        Disclosure; Page 41; 74pp; Japanese.
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                                                              Masuho Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB46868 standard; peptide; 9 AA.
(YAMA ) YAMANOUCHI PHARM CO LTD
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                                                           Hayashi K,
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Length 9; 0; Indels

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also be useful in analytical biology and molecular biology; e.g. fluorescently labeled (I) may be used as diagnostic markers or (I) may be used to prepare affinity chromatography columns for purifying integrins. DNA encoding (I) may be used for treating the same disorders as (I) itself (I) are well tolerated and have good alpha_vbeta_6-integrin
neuroprotective, alpha_vbeta_6-integrin receptor; thrombosis; tumor; cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis; osteoporosis; inflammation; infection; psoriasis; wound healing.
                                                                                                                                                                                                                                     New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections
                                                                       /note= "D-form residue"
                                                                                                                                                                                                    Jonczyk A, Diefenbach B, Goodman S;
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                          Claim 3; Page 5; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor inhibiting activity
                                                                                                                                               99DE-1033173.
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                                                                                         /label= Aee
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                                                                                 Modified-site
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                                     Synthetic
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Gaps ö Length 9; Indels 100.0%; Score 20; DB 22; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Conservative Query Match Best Local Similarity Best Loca Matches

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cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic; vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic; ophthalmological; antiarthritic; antinheumatic; antiulcer; vasotropic; neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor; cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis; osteoporosis; inflammation; infection; psoriasis; wound healing. Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic; Integrin alpha-Vbeta-6 cyclic peptide inhibitor #10. AAB46871 standard; peptide; 9 AA. (first entry) 09-MAY-2001 AAB46871; RESULT 10 AAB46871

/note= "D-form residue" Location/Qualifiers Misc-difference

Synthetic.

DE19933173-A1

Modified-site

/note= "beta alanine"

18-JAN-2001

99DE-1033173 15-JUL-1999; 99DE-1033173. 15-JUL-1999;

(MERE) MERCK PATENT GMBH.

Goodman Jonczyk A, Diefenbach B,

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WPI; 2001-192448/20.

New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections

Claim 3; Page 5; 20pp; German.

apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic retinopathy, macular degeneration, myopia, ocular histoplasmosis or rubectic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty, acute renal failure, renal inflammation or multiple sclerosis. (I) may also be useful in analytical biology and molecular biology; e.g. fluorescently labeled (I) may be used as diagnostic markers or (I) may be

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used to prepare affinity chromatography columns for purifying integrins. DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
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                                                        Length
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                                                     100.0%; Score 20; DB 22;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                                            AAB46872 standard; peptide; 9 AA.
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                itself. (I) are well tolerate
receptor inhibiting activity.
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                                                                       Conservative
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                                                       Query Match
Best Local Similarity
                                        AA;
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antinflammatory, antibacterial, antipsoriatic, vulnerary,
cerebroprotective, antitanginal, antidiabetic, ophthalmological,
antiarthritic, antitanginal, antidiabetic, ophthalmological,
antiarthritic, antitangual, antidice, vasotropic, nephrotropic,
neuroprotective. (I) are used for treating diseases involving expression
and pathological function of alpha_vbeta_6-integrin receptors, especially
thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
wound healing deficiency. Other disclosed disorders to be treated include
apoplexy, angina pectoris, ophthalmological diseases, (e.g. diabetic
retinopathy, macular degeneration, myopla, ocular histoplasmosis or
rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
acute renal failure, renal inflammation or multiple sclerosis. (I) may
also be useful in analytical biology and molecular biology; e.g.
fluorescently labeled (I) may be used as diagnostic markers or (I) may
used to prepare affinity chromatography columns for purifying integrins.
NNA encoding (I) may be used for treating the same disorders as (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 22; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB46877 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examples; Page 16; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor inhibiting activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DE-1033173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-192448/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19933173-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB46877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AAB46877
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Goodman S;

Diefenbach B,

Jonczyk A,

99DE-1033173.

15-JUL-1999;

(MERE) MERCK PATENT GMBH.

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cc residues. Cyclic peptides of formula Cyclo-(Arg-X_1-Asp-X_1-X_2-X_3-X_4-X_5-R_1) (1) and their salts and solvates. X_1 = Ser, Gly or Thr:

CC X_2 = Leu, Ile, Nle, val or Phe; X_3 = Asp, Glu, Lys or Phe; X_4 = Gly, Ala or Ser; X_5 = Leu, Ile, Nle, val or Phe; X_6 = Arg, Har or CG 1y, Ala or Ser; X_5 = Leu, Ile, Nle, val or Phe; X_6 = Arg, Har or Lys; R_1 = one or more omega-aminocarboxylic acid residues, having a coptionally derivatized and include b- as well as L-forms (in the case of optionally active aminoacids). The products of the invention have coptionally active aminoacids). The products of the invention have antiinflammatory, antibacterial, antigosoriatic, cytostatic, osteopathic, antiinflammatory, antibacterial, antigosoriatic, ophthalmological, antinflammatory, antidiabetic, ophthalmological, antinflammatory antidiabetic, ophthalmological corrective, antidiabetic, ophthalmological increaping diseases involving expression and pathological function of alpha-vbeta 6-integrin receptors, especially through of alpha-vbeta 6-integrin receptors, especially coronary heart diseases involving expression and pathological function of alpha-vbeta 6-integrin receptors, especially coronary heart disease, arteriosclerosis, thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, transpolasmosis or cumors, osteoporosis, inflammation, infection, psoriasis and wound healing deficiency other disclosed disorders to be treated include apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty, cubectic glaucoma), rheumatoid arthritis, osteopathritis, and colony; escapeorathritis, also be useful in analytical biology and molecular biology; e.g.

colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty also be useful in analytical biology and molecular biology; e.g.

colitis, crohn's disease, atherosclerosis, e.g.

colitis, crohn's disease, atherosclerosis colory e.g.

colory prepare affinity chromatography colum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic; cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic; vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic; ophthalmological; antiarthritic; antiheumatic; antiulocer; vasotropic; neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor; cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis; osteoporosis; inflammation; infection; psoriasis; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin alpha-Vbeta-6 cyclic peptide inhibitor #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 22;
100.0%; Préd. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Aha
/note= "6-aminohexanoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB46890 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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3 DLDA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB46890;
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AAB46890
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                                                                     New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin alpha-Vbeta-6 cyclic peptide inhibitor #23.
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 22;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                     Example 1; Page 11; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB46891 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                        receptor inhibiting activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                    cyclic peptides,
                                                    WPI; 2001-192448/20.
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111
3 DLDA 6
                                                                            useful e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB46891;
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AAB46892 standard; peptide; 9 AA

AAB46892

AAB46892;

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also be useful in analytical biology and molecular biology; e.g., fluorescently labeled (I) may be used as diagnostic markers or (I) may be used to prepare affinity chromatography columns for purifying integrins. DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
                                                                                                                                                                                                                                                                     This invention describes novel cyclic peptides (I), containing 8 amino acid residues and optionally further alpha, omega-aminocarboxylic acid
                                                                                                                                                                                                               New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections
                                                                     /note= "4-aminobutyric acid"
                                          'note= "D-form residue
                                                                                                                                                                               Goodman S;
                         Location/Qualifiers
                                                                                                                                                                                                                                                    Example 1; Page 11; 20pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            itself. (I) are well tolerate
receptor inhibiting activity.
                                                                                                                                         99DE-1033173.
                                                                                                                         99DE-1033173
                                                            /label- Abu
                                                                                                                                                            (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                             Diefenbach B,
                                                                                                                                                                                                WPI; 2001-192448/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
                                  Misc-difference
                                                  Modified-site
                                                                                      DE19933173-A1
                                                                                                                         15-JUL-1999;
                                                                                                                                          15-JUL-1999;
                                                                                                                                                                               Jonczyk A,
                                                                                                       18-JAN-2001
        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Gaps ; 0 Length 9; Indels 100.0%; Score 20; DB 22; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Ouery Match
Best Local Similarity 100.(
Matches 4; Conservative

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IIII DLDA 6 ô

RESULT 15

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This invention describes novel cyclic peptides (1), containing 8 amino acid residues and optionally further alpha,omega-mainocarboxylic acid residues. Cyclic peptides of formula Cyclo-(Arg-X_1-Asp-X_1-X_2-X_3-X_4-X_5-X_6-R_1) (I) and their salts and solvates. X_1 = Ser, Gly or Thr; X_2 = Leu, Ile, Nle, val or Phe; X_3 = Asp, Glu, Lys or Phe; X_4 = Gly, Ala or Ser; X_5 = Leu, Ile, Nle, val or Phe; X_6 = Arg, Har or Lys; R_1 = one or more omega-mainocarboxylic acid residues, having a length of 50-2500 mum; or is absent; the amino acid residues, having a length of 50-2500 mum; or is absent; the amino acid residues are optionally derivatized and include D- as well as L-forms (in the case of optically active aminoacids). The products of the invention have antitarterior, cardiant, antiarteriorsclerotic, cytostatic, osteopathic, antiinflammatory, antibacterial, antidabetic, opthhalmological, antianginal, antidabetic, opthhalmological, orentropic, antiinflammatory, antibacterial, antidabetic, opthhalmological, orentropic, antiinflammation, infection, psoriasis and pathological function of alpha_vbeta_6-integrin receptors, especially thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, tumors, osteopropis, other disclosed disorders to be treated include apoplexy angina pectoris, ophthalmological diseases (e.g. dlabetic rethopethy, macular degeneration, myopia, ocular histoplasmosis or rubbotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative collitis, Crohn's disease, atherosclerosis, restenosis after angioplasty, and and pathology and molecular biology; e.g. fluorescently labeled (I) may be used as diagnostic markers or (I) may eused to prepare affinity chromatography columns for purifying integrins.
                                                                                                                                                                           Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic; cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic; vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic; ophthalmological; antiarthritic; antihemmatic; antiulcer; vasotropic; neuroprotective; alpha vbeta. 6-integrin receptor; thrombosis; tumor; cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis; osteoporosis; inflammation; infection; psoriasis; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel cyclic peptides (I), containing 8 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections
                                                                                                                                  Integrin alpha-Vbeta-6 cyclic peptide inhibitor #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Abu
/note= "4-aminobutyric acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jonczyk A, Diefenbach B, Goodman S;
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 11; 20pp; German.
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                                                                                       09-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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pat943-2.rag

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Saccharomyces
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                                                                                                                                                   13-DEC-1999;
                     11-SEP-2001
                                                                                                                                                                                      Roberts GW,
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||DLDA 9
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                                                                                                                  14-JUN-2001
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     AAG87624;
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                   Saccharomyces cerevisiae; complementary peptide; peptide identification; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relavant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha_vbeta_6-integrin receptor inhibiting activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                  Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10
                                                                    Indels
                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                  Saccharomyces cerevisiae peptide, SEQ ID NO: 1310.
                                                  100.0%; Score 20; DB 22; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 22;
Pred. No. 1.4e+02;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 210; 488pp; English
                                                                                                                                              AAG86361 standard; Peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                               13-DEC-2000; 2000WO-GB04773.
                                                                                                                                                                                                                                                                                                                99GB-0029471.
                                                                                                                                                                                  (first entry)
                                                                   Conservative
                                                                                                                                                                                                                                            Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                  Heal JR;
                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEOM LTD.
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                                                         Local Similarity
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                                                                                                        cerevisiae; complementary peptide; peptide identification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and frugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from saccharomyces cerevisiae.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the identification of complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
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                                                  Saccharomyces cerevisiae peptide, SEQ ID NO: 2573.
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 384; 488pp; English.
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ilarity 100.0%;
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(first entry)
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Matches 4; Conserv
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